

OM protein - protein search, using sw model  
Run on: February 7, 2006, 16:07:31 ; Search time 204 Seconds  
(without alignments)  
1287.983 Million cell updates/sec

Title: US-10-677-669-69  
Perfect score: 3135  
Sequence: 1 MCSRVLLPLLLLLALGPG.....PLMGFGGLQSLHAKPYI 598  
Scoring table: BLOSUM62  
Searched: Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2443163  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%

Database :  
Listing first 1500 summaries

A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1

ID AAY06484 standard; protein; 598 AA.  
DE Human tumour-associated protein PRO357.  
PN WO9935170-A2.  
PD 15-JUL-1999.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 2

ID AAB01322 standard; protein; 598 AA.  
DE Human PRO357 polypeptide.  
PN WO200032776-A2.  
PD 08-JUN-2000.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 3

ID AAY93691 standard; protein; 598 AA.  
DE Amino acid sequence of novel polypeptide PRO357.  
PN WO200037640-A2.  
PD 29-JUN-2000.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 4

ID AAU83643 standard; protein; 598 AA.  
DE Human PRO protein, Seq ID No 104.  
PN WO200208288-A2.  
PD 31-JAN-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 5; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 5

ID ADY31844 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN WO200193983-A1.  
PD 13-DEC-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 5; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 6

ID ABUS5931 standard; protein; 598 AA.  
DE Human secreted/transmembrane protein PRO357.

PN US2002142959-A1.  
PD 03-OCT-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 7

ID ABU80790 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003036635-A1.  
PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 8

ID ABO33756 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003045687-A1.  
PD 06-MAR-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 9

ID ABU60241 standard; protein; 598 AA.  
DE Human PRO polypeptide #12.  
PN US2002132768-A1.  
PD 19-SEP-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 10

ID ABU64927 standard; protein; 598 AA.  
DE Human secreted/transmembrane protein PRO357.  
PN US2002173463-A1.  
PD 21-NOV-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 11

ID ABUS8361 standard; protein; 598 AA.  
DE Novel human secreted protein PRO357.  
PN US2002150976-A1.  
PD 17-OCT-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 12

ID ABUS7247 standard; protein; 598 AA.  
DE Human PRO357 protein.  
PN US2002142958-A1.  
PD 03-OCT-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 13

ID ABUS6312 standard; protein; 598 AA.  
DE Human secreted/transmembrane protein, PRO357.  
PN US2002132981-A1.  
PD 19-SEP-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 14

ID ABU60352 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2002168715-A1.  
PD 14-NOV-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 15

ID ABUS2099 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088063-A1.

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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 16
ID ABU11313 standard; protein; 598 AA.
DE Human PRO357 protein sequence.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 17
ID ABU67112 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 18
ID ABJ72279 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 19
ID ABJ72407 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 20
ID ABO34302 standard; protein; 598 AA.
DE Human secreted/transmembrane polypeptide PRO 357.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 21
ID ABJ72109 standard; protein; 598 AA.
DE Human membrane bound receptor/protein PRO357 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 22
ID ADB83594 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 23
ID ADB80700 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 24
ID ADB73241 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 25
ID ADB78323 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 26
ID ADB84971 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 27
ID ADB78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 28
ID ADB87143 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 29
ID ADB84725 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 30
ID ADB83840 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 31
ID ADB72995 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 32
ID ADC25825 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 33
ID ADC25583 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002156004-A1.
PD 24-OCT-2002.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 34  
ID ADC25704 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003077698-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 35  
ID ADC36833 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 36  
ID ADC21823 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 37  
ID ADC49854 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 38  
ID ADC49053 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 39  
ID ADC49570 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 40  
ID ADC47431 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 41  
ID ADC47176 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 42  
ID ADC78051 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 43  
ID ADD06286 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 44  
ID ADC77805 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 45  
ID ADD50768 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 46  
ID ADD51014 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 47  
ID ADD50495 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 48  
ID ADD50249 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 49  
ID ADD51260 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 50  
ID ADH27489 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003083479-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 51  
ID ADC48807 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

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RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 54
ID ADD75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 55
ID ADD75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 56
ID ADD85029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 57
ID ADD86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 58
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 59
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 61
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 62
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 70
ID ADD85535 standard; protein; 598 AA.
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DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 71  
ID ADE05084 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 72  
ID ADD75297 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 73  
ID ADD76841 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 74  
ID ADD86609 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 75  
ID ADD78077 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 76  
ID ADE71538 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003096742-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 77  
ID ADD77585 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 78  
ID ADD77831 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 79  
ID ADD85289 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.

PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 80  
ID ADD73821 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 81  
ID ADD74559 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 82  
ID ADD77087 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 83  
ID ADD85781 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 84  
ID ADE05330 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 85  
ID ADD74805 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 86  
ID ADG05617 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 87  
ID ADG27171 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 88  
ID ADG11234 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096967-A1.

PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 89  
ID ADG12013 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 90  
ID ADF94570 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 91  
ID ADG6666 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 92  
ID ADG63481 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003211570-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 93  
ID ADH39010 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 94  
ID ADH43210 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003207401-A1  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 95  
ID ADG34100 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 96  
ID ADI33570 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 97  
ID ADH9664 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2004019183-A1.  
PD 29-JAN-2004.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 98  
ID ADI29825 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 99  
ID ADM27222 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 100  
ID ADK66580 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 101  
ID ADN00448 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2004091972-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 102  
ID ADU25372 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2004220385-A1.  
PD 04-NOV-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 103  
ID ADY39535 standard; protein; 598 AA.  
DE Human insulin-like growth factor homolog PRO357 precursor protein.  
PN US2005048613-A1.  
PD 03-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 9; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 104  
ID ADY73816 standard; protein; 598 AA.  
DE Human PRO357 protein, SEQ ID NO: 69.  
PN US2005059115-A1.  
PD 17-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 9; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.8e-190;  
RESULT 105  
ID AAV17831 standard; protein; 598 AA.  
DE Human PRO357 protein sequence.  
PN WO9928462-A2.  
PD 10-JUN-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 3126; DB 2; Length 598;  
Best Local Similarity 99.8%; Pred. No. 1.4e-189;  
RESULT 106  
ID AAB07428 standard; protein; 673 AA.  
DE Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).  
PN WO20042170-A1.  
PD 20-JUL-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Query Match 98.4%; Score 3083.5; DB 3; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 107  
ID AAB87533 standard; protein; 673 AA.  
DE Human PRO1282.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 4; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 108  
ID AAB6166 standard; protein; 673 AA.  
DE Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 4; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 109  
ID RAU75266 standard; protein; 673 AA.  
DE Human Slit-like protein #1.  
PN WO200212346-A2.  
PD 14-FEB-2002.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 110  
ID ABG95858 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 111  
ID ABG78042 standard; protein; 673 AA.  
DE Human leucine-rich surface glycoprotein (LRSG-1).  
PN US2002072089-A1.  
PD 13-JUN-2002.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (MACB/) MACBETH K J.  
PA (BUSF/) BUSFIELD S J.  
PA (PANY/) PAN Y.  
PA (WHIT/) WHITE D.  
PA (KHOD/) KHODADOUST M M.  
PA (GUWW/) GU W.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 112  
ID ABUS7981 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 113  
ID ABUS9059 standard; protein; 673 AA.  
DE Novel human secreted or transmembrane protein PRO1282.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 114  
ID ABUS2571 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 115  
ID ABUS9206 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, #19.

DE Human secreted/transmembrane protein, #19.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 116  
ID ABUI3872 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2002101125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 117  
ID ABU72457 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 118  
ID ABUS9083 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 119  
ID ABO33942 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 120  
ID ABU71959 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 121  
ID ABU71513 standard; protein; 673 AA.  
DE Human secreted polypeptide PRO1282.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 122  
ID ABU72294 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 123  
ID ABUS9067 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 124  
ID ABUS9206 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, #19.

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PN US2003027162-A1.
PD 06-FEB-2003.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 125
ID ABO25903 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 126
ID ABO27288 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 127
ID ABO2483 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 128
ID ABO81153 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 129
ID ABO33268 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 130
ID ABUS8912 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 131
ID ABUS2290 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 132
ID ABUS9355 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 133
ID ABUS9270 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 134
ID ABUS9275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 135
ID ABUS2482 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 136
ID ABUS2121 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 137
ID ABUS6446 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 138
ID ABUI0827 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 139
ID ABUS1579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 140
ID ABU72116 standard; protein; 673 AA.
DE Human PRO polypeptide #9.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 141
ID ABUS8518 standard; protein; 673 AA.
DE Human secreted and transmembrane polypeptide PRO1282.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 142
ID ABO34032 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match      98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 143
ID ADB17073 standard; protein; 673 AA.
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DE Human transmembrane PRO polypeptide (SeqID 16).  
PN US2003050462-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 144  
ID ADA37563 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 145  
ID ADA21249 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO1282.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 146  
ID ABO44246 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO 1282.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 147  
ID ADA10036 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, PRO1282.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 148  
ID ADA19878 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 149  
ID ADB17261 standard; protein; 673 AA.  
DE Human transmembrane PRO polypeptide (SeqID 16).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 150  
ID ADA17580 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 151  
ID ADA27688 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 152  
ID ADA20050 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 153  
ID ABO34174 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO 1282.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 154  
ID ADA94268 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 155  
ID ADA38493 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 156  
ID ADA32614 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 157  
ID ADA00347 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO 1282.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 158  
ID ABO33118 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 159  
ID ADA22175 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO1282.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 160  
ID ABO22488 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 161  
ID ADA06341 standard; protein; 673 AA.  
DE Human secreted/transmembrane PRO polypeptide #13.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 162  
ID ADA39034 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;

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RESULT 163
ID ADB95589 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 164
ID ADB96060 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 165
ID ADB68268 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 166
ID ADB68075 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 167
ID ADB90892 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 168
ID ADC57532 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 169
ID ADC54896 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 170
ID ADC11763 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 171
ID ADC06972 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 172
ID ADC56185 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 173
ID ADC17151 standard; protein; 673 AA.
DE Mammalian PRO polypeptide (segID 16).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 174
ID ADC07240 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003068447-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 175
ID ADC11230 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 176
ID ADC14849 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 177
ID ADC52344 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 178
ID ADC14352 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 179
ID ADD07884 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 180
ID ADC81709 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 181
ID ADD07351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 182
ID ADC82242 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059833-A1.
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PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 183  
ID ADD08422 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 184  
ID ADD06671 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 185  
ID ADC82918 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
FN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 186  
ID ADD55025 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
FN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 187  
ID ADD36020 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 188  
ID ADD55983 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
FN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 189  
ID ADD54421 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
FN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 190  
ID ADE26575 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 191  
ID ADE26042 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 192  
ID ADF66979 standard; protein; 673 AA.  
DE Human PRO1282 amino acid sequence SEQ ID NO:52.  
FN US2002198148-A1.

PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 193  
ID ADG01021 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 194  
ID ADG08574 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 195  
ID ADF95195 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 196  
ID ADH24048 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 197  
ID ADH34074 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 198  
ID ADH29907 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 199  
ID ADH23878 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 200  
ID ADG85282 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 201  
ID ADH24558 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
FN US2003180907-A1.  
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 202
ID ADH37414 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 203
ID ADH02003 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 204
ID ADH37584 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 205
ID ADG85622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 206
ID ADH24218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 207
ID ADH38512 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 208
ID ADG83633 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 209
ID ADH29441 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 210
ID ADH27557 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 211
ID ADH37754 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 212
ID ADH37931 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 213
ID ADH57351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 214
ID ADH53493 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 215
ID ADH53663 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 216
ID ADH51999 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 217
ID ADH49854 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 218
ID ADI25364 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 219
ID ADH90157 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
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Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 220  
ID ADI25534 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 221  
ID ADH97708 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 222  
ID ADH97708 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 223  
ID ADI35233 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 224  
ID ADI3556 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 225  
ID ADH9987 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 226  
ID ADH99725 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 227  
ID ADH98388 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 228  
ID ADI11063 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 229  
ID ADI11573 standard; protein; 673 AA.

DE Human PRO polypeptide #8.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 230  
ID ADH98218 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 231  
ID ADH98558 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 232  
ID ADH98048 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 233  
ID ADI05036 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 234  
ID ADI03386 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 235  
ID ADI04781 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 236  
ID ADH78235 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181688-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 237  
ID ADI19579 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 238  
ID ADH90327 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.

PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 239  
ID ADI03046 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 240  
ID ADH77895 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 241  
ID ADH97878 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 242  
ID ADI01263 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 243  
ID ADI01958 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 244  
ID ADI03216 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 245  
ID ADI11403 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 246  
ID ADI02305 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 247  
ID ADI11743 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181685-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 248  
ID ADI05380 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 249  
ID ADH79452 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 250  
ID ADI19409 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 251  
ID ADI05210 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 252  
ID ADH79622 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 253  
ID ADI01448 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 254  
ID ADI01618 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 255  
ID ADI01788 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 256  
ID ADH79792 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191289-A1.  
PD 09-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 257  
ID ADI04610 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 258  
ID ADI02746 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 259  
ID ADH78065 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 260  
ID ADI25704 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 261  
ID ADI25874 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 262  
ID ADK65386 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 263  
ID ADH98728 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 264  
ID ADH79969 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 265  
ID ADL93700 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.

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Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 266  
ID ADC52154 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 267  
ID ADF35178 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 268  
ID ADG11428 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 269  
ID ADH06586 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 270  
ID ADH06416 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 271  
ID ADG68837 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 272  
ID ADH27727 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 273  
ID ADH25068 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 274  
ID ADH33700 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.1e-187;  
RESULT 275  
ID ADL93700 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.



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DE Human secreted/transmembrane protein PRO1282.
PD US2003224358-A1.
PD 04-DEC-2003.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 294
ID ADH02173 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PD US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 295
ID ADG69177 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 296
ID ADG85962 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 297
ID ADH24898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 298
ID ADH39515 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 299
ID ADH19831 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PD US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 300
ID ADH02513 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PD US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 301
ID ADG69007 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 302
ID ADH07610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180850-A1.
PD 25-SEP-2003.
DE Human secreted/transmembrane protein PRO1282.
PD US2003224358-A1.
PD 04-DEC-2003.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 303
ID ADG86132 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 304
ID ADH24728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 305
ID ADH25776 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 306
ID ADH38342 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 307
ID ADH57181 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 308
ID ADH52169 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 309
ID ADH49535 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 310
ID ADH90497 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 311
ID ADH11233 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PD US2003181683-A1.
PD 25-SEP-2003.
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PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 312
ID ADH98898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 313
ID ADI02128 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 314
ID ADH98667 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 315
ID ADJ98542 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 316
ID ADJ98712 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 317
ID ADH78871 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 318
ID ADJ99105 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 319
ID ADJ99275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 320
ID ADJ98893 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 321
ID ADH79041 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 322
ID ADK00901 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 323
ID ADK1422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 324
ID ADM80871 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 325
ID ADR45587 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 326
ID ADY77711 standard; protein; 673 AA.
DE Neoplastic disease detection protein PRO1282.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 327
ID AEA38367 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #81.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 328
ID AAB84689 standard; protein; 673 AA.
DE Amino acid sequence of human slit polypeptide zslit3.
PN WO200146418-A1.
PD 28-JUN-2001.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match 98.2%; Score 3078.5; DB 4; Length 673;
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Best Local Similarity 88.6%; Pred. No. 1.7e-186;  
RESULT 329  
ID ADF69108 standard; protein; 673 AA.  
DE Human MP53 protein sequence SEQ ID NO:78.  
PN WO2003083047-A2.  
PD 09-OCT-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 98.2%; Score 3078.5; DB 7; Length 673;  
Best Local Similarity 88.6%; Pred. No. 1.7e-186;  
RESULT 330  
ID ABO59449 standard; protein; 676 AA.  
DE Human genome derived single exon protein #5683.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 98.2%; Score 3078.5; DB 8; Length 676;  
Best Local Similarity 88.6%; Pred. No. 1.7e-186;  
RESULT 331  
ID ADA57213 standard; protein; 672 AA.  
DE Human secreted protein #496.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.1e-177;  
RESULT 332  
ID ADA41092 standard; protein; 672 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.1e-177;  
RESULT 333  
ID ABR47923 standard; protein; 672 AA.  
DE Human secreted protein, SEQ ID 814.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.8%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.1e-177;  
RESULT 334  
ID AAB38323 standard; protein; 673 AA.  
DE Human secreted protein encoded by gene 3 clone HSYAV50.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 3; Length 673;  
Best Local Similarity 85.2%; Pred. No. 2.1e-177;  
RESULT 335  
ID AAB38400 standard; peptide; 723 AA.  
DE Fragment of human secreted protein encoded by gene 3 clone HSYAV50.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 3; Length 723;  
Best Local Similarity 85.2%; Pred. No. 2.2e-177;  
RESULT 336  
ID AAU75267 standard; protein; 630 AA.  
DE Human Slit-like protein #2.  
PN WO200212346-A2.  
PD 14-FEB-2002.  
PA (PHAA-) PHARMACIA CORP.  
Query Match 90.8%; Score 2845.5; DB 5; Length 630;  
Best Local Similarity 85.2%; Pred. No. 8.9e-172;  
RESULT 337  
ID AAY66643 standard; protein; 611 AA.  
DE Membrane-bound protein PRO1282.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH-) GENENTECH INC.  
Query Match 15.0%; Score 471; DB 7; Length 117;  
Query Match 86.5%; Score 2712.5; DB 3; Length 611;  
Best Local Similarity 79.5%; Pred. No. 2.3e-163;  
RESULT 338  
ID ABG78046 standard; protein; 673 AA.  
DE Mouse leucine-rich surface glycoprotein (LRSG-1).  
PN US2002072089-A1.  
PD 13-JUN-2002.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (MACE/) MACBETH K J.  
PA (BUSF/) BUSFIELD S J.  
PA (PANIT/) PAN Y.  
PA (WHIT/) WHITE D.  
PA (KHOD/) KHODADOUST M M.  
PA (GUWW/) GU W.  
Query Match 79.4%; Score 2490; DB 5; Length 673;  
Best Local Similarity 73.5%; Pred. No. 3.2e-149;  
RESULT 339  
ID ADR45596 standard; protein; 673 AA.  
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #2.  
PN US2004176296-A1.  
PD 09-SEP-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 79.4%; Score 2490; DB 8; Length 673;  
Best Local Similarity 73.5%; Pred. No. 3.2e-149;  
RESULT 340  
ID ADA00753 standard; protein; 673 AA.  
DE Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.  
PN WO2003018805-A1.  
PD 06-MAR-2003.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
PA (NINA-) JAPAN NAT CANCER CENT.  
Query Match 79.2%; Score 2484; DB 6; Length 673;  
Best Local Similarity 73.4%; Pred. No. 7.7e-149;  
RESULT 341  
ID AAB07431 standard; protein; 493 AA.  
DE A leucine-rich surface glycoprotein (LRSG).  
PN WO200042170-A1.  
PD 20-JUL-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 53.3%; Score 1672; DB 3; Length 493;  
Best Local Similarity 53.3%; Pred. No. 1.5e-97;  
RESULT 342  
ID ABB72324 standard; protein; 281 AA.  
DE Rat protein isolated from skin cells SEQ ID NO: 648.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 37.6%; Score 1178.5; DB 5; Length 281;  
Best Local Similarity 80.7%; Pred. No. 1.4e-66;  
RESULT 343  
ID AAO30403 standard; protein; 311 AA.  
DE Human secreted protein (SECP)-6.  
PN WO2003046196-A1.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.8%; Score 997.5; DB 7; Length 311;  
Best Local Similarity 68.7%; Pred. No. 4.6e-55;  
RESULT 344  
ID ABR58506 standard; protein; 307 AA.  
DE Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.  
PN WO2003029437-A2.  
PD 10-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.3%; Score 980.5; DB 6; Length 307;  
Best Local Similarity 67.9%; Pred. No. 5.5e-54;  
RESULT 345  
ID AAO30821 standard; protein; 117 AA.  
DE Human cell adhesion and extracellular matrix protein (CAECM)-11.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.0%; Score 471; DB 7; Length 117;

Best Local Similarity 98.9%; Pred. No. 3.4e-22;  
RESULT 346  
ID AAE23980 standard; protein; 635 AA.  
DE Human Lp220 secreted protein.  
PN WO200226801-A2.  
PD 04-APR-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 11.5%; Score 360.5; DB 5; Length 635;  
Best Local Similarity 27.1%; Pred. No. 2.4e-14;  
RESULT 347  
ID ABP70142 standard; protein; 647 AA.  
DE Human NOV44a.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.5%; Score 360.5; DB 5; Length 647;  
Best Local Similarity 27.1%; Pred. No. 2.5e-14;  
RESULT 348  
ID AAO26256 standard; protein; 635 AA.  
DE MDDT related human protein SEQ ID No 34.  
PN WO200296951-A1.  
PD 05-DEC-2002.  
PA (INCV-) INCVTE GENOMICS INC.  
Query Match 11.5%; Score 359.5; DB 6; Length 635;  
Best Local Similarity 27.6%; Pred. No. 2.8e-14;  
RESULT 349  
ID ADZ09859 standard; protein; 635 AA.  
DE Human breast cancer marker MGC3103 protein.  
PN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB ) BAYER HEALTHCARE AG.  
Query Match 11.5%; Score 359.5; DB 9; Length 635;  
Best Local Similarity 27.6%; Pred. No. 2.8e-14;  
RESULT 350  
ID ABP70144 standard; protein; 778 AA.  
DE Human NOV44c.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.4%; Score 357.5; DB 5; Length 778;  
Best Local Similarity 26.7%; Pred. No. 4.8e-14;  
RESULT 351  
ID ADM90979 standard; protein; 545 AA.  
DE Human pharmaceutically useful protein SeqID 372.  
PN WO2004020595-A2.  
PD 11-MAR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Query Match 11.2%; Score 350.5; DB 8; Length 545;  
Best Local Similarity 27.9%; Pred. No. 8.7e-14;  
RESULT 352  
ID ABP70143 standard; protein; 566 AA.  
DE Human NOV44b.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.8%; Score 339; DB 5; Length 566;  
Best Local Similarity 26.9%; Pred. No. 4.9e-13;  
RESULT 353  
ID AAE17484 standard; protein; 551 AA.  
DE Human leucine-rich repeat-8 (ZLR8) protein #2.  
PN WO200202604-A2.  
PD 10-JAN-2002.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 10.8%; Score 338; DB 5; Length 551;  
Best Local Similarity 27.4%; Pred. No. 5.5e-13;  
RESULT 354  
ID ADI21104 standard; protein; 618 AA.  
DE Novel human prodein #79.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.

Query Match 10.7%; Score 337; DB 7; Length 618;  
Best Local Similarity 27.2%; Pred. No. 7.2e-13;  
RESULT 355  
ID ADA23287 standard; protein; 653 AA.  
DE Human SECX polypeptide, SEC5 #1.  
PN US2003054514-A1.  
PD 20-MAR-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (LARO/) LAROCHELLE W J.  
Query Match 10.7%; Score 337; DB 6; Length 653;  
Best Local Similarity 23.6%; Pred. No. 7.7e-13;  
RESULT 356  
ID AAB23033 standard; protein; 694 AA.  
DE Human SLIT protein-like splice variant, SECX 3352358-1.  
PN WO200053742-A2.  
PD 14-SEP-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.7%; Score 337; DB 3; Length 694;  
Best Local Similarity 23.6%; Pred. No. 8.3e-13;  
RESULT 357  
ID AAB23034 standard; protein; 590 AA.  
DE Human SLIT protein-like splice variant, SECX 3352358-2.  
PN WO200053742-A2.  
PD 14-SEP-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.6%; Score 333; DB 3; Length 590;  
Best Local Similarity 25.8%; Pred. No. 1.2e-12;  
RESULT 358  
ID ADA23289 standard; protein; 590 AA.  
DE Human SECX polypeptide, SEC6.  
PN US2003054514-A1.  
PD 20-MAR-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (LARO/) LAROCHELLE W J.  
Query Match 10.6%; Score 333; DB 6; Length 590;  
Best Local Similarity 25.8%; Pred. No. 1.2e-12;  
RESULT 359  
ID ABG04827 standard; protein; 526 AA.  
DE Novel human diagnostic protein #4818.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.6%; Score 332; DB 4; Length 526;  
Best Local Similarity 26.9%; Pred. No. 1.2e-12;  
RESULT 360  
ID AAY28806 standard; protein; 653 AA.  
DE cc359.4 secreted protein.  
PN WO9950405-A1.  
PD 07-OCT-1999.  
PA (GENY ) GENETICS INST INC.  
Query Match 10.5%; Score 330; DB 2; Length 653;  
Best Local Similarity 24.2%; Pred. No. 2.1e-12;  
RESULT 361  
ID AAY66694 standard; protein; 653 AA.  
DE Membrane-bound protein PRO1111.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 3; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 362  
ID AAB24073 standard; protein; 653 AA.  
DE Human PRO1111 protein sequence SEQ ID NO.46.  
PN WO200053755-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 3; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 363  
ID AAU12390 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.

PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 4; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 364  
ID AAE09438 standard; protein; 653 AA.  
DE Human sbgPRO331a protein.  
PN WO200160850-A1.  
PD 23-AUG-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (GETH ) SMITHKLINE BEECHAM PLC.  
Query Match 10.5%; Score 330; DB 4; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 365  
ID AAB65217 standard; protein; 653 AA.  
DE Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.  
PN WO2000073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 4; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 366  
ID ABUS8032 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 367  
ID ABUS9110 standard; protein; 653 AA.  
DE Novel human secreted or transmembrane protein PRO1111.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 368  
ID ABUS82622 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 369  
ID ABO17834 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 370  
ID ABUS60541 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, #93.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 371  
ID ABUS1923 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 372  
ID ABUS1088 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 373  
ID ABUS2508 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 374  
ID ABUS66788 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 375  
ID AAO23105 standard; protein; 653 AA.  
DE NAG14 'human modifier of p53 pathway' protein.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 376  
ID ABUS9869 standard; protein; 653 AA.  
DE Novel secreted and transmembrane protein PRO1111.  
PN US2003017583-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 377  
ID ABUS9257 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, #93.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 378  
ID ABO25954 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 379  
ID ABO25059 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein (PRO) #219.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 380  
ID ABUS8963 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, #93.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 381  
ID ABUS2341 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US200302187-A1.  
PD 30-JAN-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 382  
ID ABUS9406 standard; protein; 653 AA.

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DE Novel human secreted or transmembrane protein PRO1344.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 383
ID ABU67064 standard; protein; 653 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 438.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 384
ID ABU92172 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 385
ID ABU10878 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 386
ID ABU81630 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 387
ID ABU88569 standard; protein; 653 AA.
DE Human secreted and transmembrane polypeptide PRO1111.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 388
ID ABO34083 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 389
ID ADA45957 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003023228-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 390
ID ADA76388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 391
ID ADA19038 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 392
ID ADA61661 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 393
ID ADB19446 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 394
ID ADB27987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 395
ID ADA86466 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 396
ID ADB16030 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 397
ID ADA37740 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 398
ID ADA47816 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 399
ID ADA21426 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 400
ID ADA10213 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, PRO1111.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 401
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ID ADA67611 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 402  
ID ADB30618 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 403  
ID ADA85914 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 404  
ID ADA17757 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 405  
ID ADA97126 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 406  
ID ADA79430 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 407  
ID ADA87569 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 408  
ID ADB16771 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 409  
ID ADA27865 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 410  
ID ADA91863 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082694-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 411  
ID ADB14926 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 412  
ID ADB18887 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 413  
ID ADA94102 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 414  
ID ADB19998 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 415  
ID ADB13310 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 416  
ID ABO43367 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 417  
ID ADA94445 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 418  
ID ADA74564 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 419  
ID ADB24797 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 420
ID ADA82321 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 421
ID ADA75284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 422
ID ADA85362 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 423
ID ADA84810 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 424
ID ADB30066 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 425
ID ADA80594 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 426
ID ADA75836 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 427
ID ADA38670 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 428
ID ADA47061 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 429
ID ADA96022 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 430
ID ADA93533 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 431
ID ADB26883 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 432
ID ADB31170 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 433
ID ADA92791 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 434
ID ADA61098 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 435
ID ADB24245 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 436
ID ADA96574 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 437
ID ADA81146 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 438
ID ADA96022 standard; protein; 653 AA.
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DE Human PRO polypeptide #219.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 439  
ID ADB26331 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 440  
ID ADB21816 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 441  
ID ADA77595 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068787-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 442  
ID ADB18335 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003077110-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 443  
ID ADA87018 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 444  
ID ADA88121 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 445  
ID ADA46509 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 446  
ID ADB28539 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 447  
ID ADB29091 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.

PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 448  
ID ABO53169 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 449  
ID ADA77043 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 450  
ID ADA22352 standard; protein; 653 AA.  
DE Human secreted/transmembrane polypeptide PRO1111.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 451  
ID ADA88673 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 452  
ID ADA37678 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 453  
ID ADB27435 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 454  
ID ADB22368 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 455  
ID ABO22539 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 456  
ID ADA06518 standard; protein; 653 AA.  
DE Human secreted/transmembrane PRO polypeptide #64.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 457  
ID ADA39211 standard; protein; 653 AA.

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DE Human secreted/transmembrane protein PRO1111.
PN US2003059782-A1.
PD 27-MAR-2003.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 458
ID ADA67059 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 459
ID ADB22920 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 460
ID ADB23693 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 461
ID ADA92415 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 462
ID ADB15478 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 463
ID ADB38730 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 464
ID ADB96237 standard; protein; 653 AA.
DE Human PRO polypeptide #84.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 465
ID ADB38178 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 466
ID ADB66650 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 467
ID ADB89730 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 468
ID ADB90462 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 469
ID ADB39563 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 470
ID ADB47186 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 471
ID ADB86793 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 472
ID ADB77398 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 473
ID ADB34555 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 474
ID ADB35659 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 475
ID ADB34003 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 476  
ID ADB35107 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 477  
ID ADB36211 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 478  
ID ADB46606 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 479  
ID ADC57709 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 480  
ID ADC55073 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 481  
ID ADC11940 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 482  
ID ADC56362 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 483  
ID ADC07417 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 484  
ID ADC11407 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 485  
ID ADC50479 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092106-A1.  
PD 15-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 486  
ID ADC72026 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 487  
ID ADC60005 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 488  
ID ADC53012 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 489  
ID ADC57366 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 490  
ID ADC60557 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 491  
ID ADC51032 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 492  
ID ADC65559 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 493  
ID ADC54657 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 494  
ID ADC53618 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 495
ID ADCS59141 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 496
ID ADC56019 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 497
ID ADC58589 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 498
ID ADC14529 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 499
ID ADD08061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 500
ID ADD03263 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 501
ID ADC90255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 502
ID ADC81886 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 503
ID ADC69674 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 504
ID ADC48563 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.
PD 08-MAY-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 505
ID ADD10092 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 506
ID ADD07528 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 507
ID ADD04667 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 508
ID ADC82419 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 509
ID ADC90623 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 510
ID ADD11130 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 511
ID ADC48011 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 512
ID ADD08599 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 513
ID ADC80071 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.
PD 08-MAY-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 514  
ID ADD06848 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 515  
ID ADD09540 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 516  
ID ADC83095 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 517  
ID ADD41253 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 518  
ID ADD52392 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 519  
ID ADD53132 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 520  
ID ADD53684 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 521  
ID ADD55202 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 522  
ID ADD56160 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 523  
ID ADD51840 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 524  
ID ADD02639 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 525  
ID ADD02073 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 526  
ID ADD54255 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 527  
ID ADD54598 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 528  
ID ADD52572 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 529  
ID ADD91468 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 530  
ID ADE04082 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 531  
ID ADE26752 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 532  
ID ADE32379 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.

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PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 533
ID ADE22311 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 534
ID ADD79535 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 535
ID ADE42071 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 536
ID ADE17888 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 537
ID ADD92020 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 538
ID ADE33483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 539
ID ADE34035 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 540
ID ADD80087 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 541
ID ADD93124 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 542
ID ADE19544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 543
ID ADE18992 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 544
ID ADE43188 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 545
ID ADD95977 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 546
ID ADE22863 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 547
ID ADD78981 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 548
ID ADE26219 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 549
ID ADE32931 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 550
ID ADE42623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
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Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 551
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 552
ID ADG80667 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 553
ID ADE40951 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 554
ID ADE04750 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 555
ID ADE92879 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 556
ID ADF67156 standard; protein; 653 AA.
DE Human PRO1111 amino acid sequence SEQ ID NO:229.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 557
ID ADG21588 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 558
ID ADG23229 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 559
ID ADP97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 560
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 561
ID ADG80076 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 562
ID ADH55368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 563
ID ADH55920 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 564
ID ADI35410 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 565
ID ADI64139 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 566
ID ADI65088 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 567
ID ADI63587 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 568
ID ADH82001 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 569
ID ADP97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 570
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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ID ADH99902 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003049682-A1.
PD 13-MAR-2003.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 570
ID ADH81449 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 571
ID ADM82618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 572
ID ADN16017 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 573
ID ADN16646 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 574
ID ADN15465 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 575
ID ADN14913 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 576
ID ADC81175 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 577
ID ADD76623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 578
ID ADD87987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199054-A1.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 580
ID ADE75839 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 581
ID ADE23415 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 582
ID ADE23967 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 583
ID ADE24610 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 584
ID ADD87435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 585
ID ADE89301 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 586
ID ADE18440 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 587
ID ADE88749 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199054-A1.
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Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 606
ID ADG16824 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 607
ID ADG95283 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 608
ID ADG19550 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 609
ID ADG13387 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 610
ID ADG08444 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 611
ID ADG15614 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 612
ID ADF97012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 613
ID ADG06197 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 614
ID ADG21781 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 615
ID ADG04070 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 616
ID ADG24971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 617
ID ADG07268 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 618
ID ADG07820 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 619
ID ADG55315 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 620
ID ADG60979 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 621
ID ADG62083 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 622
ID ADG82284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 623
ID ADG57523 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 624
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ID ADG56971 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 625  
ID ADG55867 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 626  
ID ADG58627 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 627  
ID ADG70993 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 628  
ID ADG58075 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 629  
ID ADG53659 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 630  
ID ADG71545 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 631  
ID ADG81732 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 632  
ID ADH19475 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 633  
ID ADH30694 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.

PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 634  
ID ADH12061 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 635  
ID ADG52483 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 636  
ID ADG54211 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 637  
ID ADG81180 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 638  
ID ADG56419 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 639  
ID ADH12685 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 640  
ID ADH20968 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 641  
ID ADG61531 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 642  
ID ADH20008 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003219856-A1.  
PD 27-NOV-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 643
ID ADH28618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 644
ID ADG54763 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 645
ID ADG59803 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 646
ID ADI81227 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 647
ID ADG09970 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 648
ID ADI15441 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 649
ID ADG09318 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 650
ID ADI14773 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 651
ID ADI18368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 652
ID ADJ63649 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US20040319164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 653
ID ADJ77544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 654
ID ADJ65666 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 655
ID ADM27802 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 656
ID ADM42526 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 657
ID ADM28388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 658
ID ADI95870 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 659
ID ADI96422 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 660
ID ADS32374 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
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Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 661  
ID ADT03358 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004214269-A1.  
PD 28-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 662  
ID ADZ03409 standard; protein; 653 AA.  
DE Human secreted/transmembrane PRO1111 protein.  
PN US2005074837-A1.  
PD 07-APR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 663  
ID AEA38492 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, #132.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 664  
ID AEA23332 standard; protein; 653 AA.  
DE Tumor antigen of hematopoietic origin TAHO15.  
PN WO2005049075-A2.  
PD 02-JUN-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 665  
ID ABB14155 standard; protein; 653 AA.  
DE Cancer cell diagnosis method-related human protein - SEQ ID 438.  
PN US2005153396-A1.  
PD 14-JUL-2005.  
PA (BAKE/) BAKER K P.  
PA (BERE/) BERESINI M.  
PA (DERO/) DEFORGE L.  
PA (DESN/) DESNOYERS L.  
PA (FILV/) FILVAROFF E.  
PA (GAOW/) GAO W.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (SHER/) SHERWOOD S.  
PA (SMIT/) SMITH V.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
PA (ZHAN/) ZHANG Z.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.1e-12;  
RESULT 666  
ID ABU12069 standard; protein; 775 AA.  
DE Human NOV15a CG92531-01 protein SEQ ID 58.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.5%; Score 329.5; DB 6; Length 775;  
Best Local Similarity 26.0%; Pred. No. 2.8e-12;  
RESULT 667  
ID ABG98014 standard; protein; 649 AA.  
DE Human leucine rich repeat domain protein associated protein #1.  
PN WO200274959-A2.  
PD 26-SEP-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.5%; Score 329; DB 5; Length 649;  
Best Local Similarity 24.6%; Pred. No. 2.5e-12;

RESULT 668  
ID ADS98753 standard; protein; 824 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 1017.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA/) DRVANAC R T.  
Query Match 10.5%; Score 329; DB 8; Length 824;  
Best Local Similarity 25.5%; Pred. No. 3.3e-12;  
RESULT 669  
ID AEG34079 standard; protein; 627 AA.  
DE Human PRO peptide #51.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 5; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 670  
ID ADA01368 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 671  
ID ADA43797 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 672  
ID ADA43565 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003073196-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 673  
ID ADA01240 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068782-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 674  
ID ADA01124 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 675  
ID ADA01124 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 676  
ID ADA43681 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003073190-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 677  
ID ADA06943 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;

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RESULT 677
ID ADA08431 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 678
ID ADB99724 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 679
ID ADB87007 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 680
ID ADB66162 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 681
ID ADB99840 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 682
ID ADB99495 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 683
ID ADB66046 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 684
ID ADC23444 standard; protein; 627 AA.
DE Human transmembrane PRO polypeptide (SeqID 100) .
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 685
ID ADC26137 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 686
ID ADG06546 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 687
ID ADE11270 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 688
ID ADD88201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 689
ID ADD95496 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 690
ID ADE06426 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 691
ID ADE38201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 692
ID ADD88317 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 693
ID ADD90898 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 694
ID ADF99453 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 695
ID ADG06546 standard; protein; 627 AA.
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DE Human PRO polypeptide #50.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 696  
ID ADG05497 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 697  
ID ADG82498 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 698  
ID ADE51751 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 699  
ID ADE51867 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 700  
ID ADE37725 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104584-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 701  
ID ADE37609 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 702  
ID ADD95380 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 703  
ID ADE38080 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003104586-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 704  
ID ADE76169 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.

PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 705  
ID ADE39492 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 706  
ID ADE04296 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 707  
ID ADE39893 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 708  
ID ADE19758 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 709  
ID ADE77336 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 710  
ID ADE65444 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 711  
ID ADE76053 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003124663-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 712  
ID ADE37964 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 713  
ID ADE64574 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119114-A1.

PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 714  
ID ADE38909 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 715  
ID ADE31983 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 716  
ID ADD91014 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 717  
ID ADE38793 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 718  
ID ADE37493 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 719  
ID ADE06309 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 720  
ID ADD90169 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 721  
ID ADE38677 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 722  
ID ADE39608 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119118-A1.  
PD 26-JUN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 723  
ID ADD89213 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 724  
ID ADD88980 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 725  
ID ADE19874 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 726  
ID ADE77452 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 727  
ID ADE65328 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 728  
ID ADE39376 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 729  
ID ADE38561 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 730  
ID ADG11114 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 731  
ID ADG10998 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 732  
ID ADH31526 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 733  
ID ADH38774 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 734  
ID ADH29409 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 735  
ID ADH23712 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 736  
ID ADH27042 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 737  
ID ADH38310 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 738  
ID ADH26926 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 739  
ID ADH38194 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 740  
ID ADH38890 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;

Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 741  
ID ADH23828 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 742  
ID ADH40203 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 743  
ID ADH40088 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 744  
ID ADH31410 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 745  
ID ADH29288 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 746  
ID ADH49503 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 747  
ID ADH51967 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 748  
ID ADH49822 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 749  
ID ADH52423 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;

RESULT 750  
ID ADH52539 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 751  
ID ADH58536 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 752  
ID ADH51851 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 753  
ID ADH58412 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 754  
ID ADI13609 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 755  
ID ADK00865 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 756  
ID ADL08606 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.5e-12;  
RESULT 757  
ID AAU32870 standard; protein; 636 AA.  
DE Novel human secreted protein #3361.  
PN WO20017949-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.4%; Score 327.5; DB 4; Length 636;  
Best Local Similarity 24.2%; Pred. No. 3e-12;  
RESULT 758  
ID ABO84499 standard; protein; 626 AA.  
DE Mouse cancer-associated protein MP14-035.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.3%; Score 324; DB 8; Length 626;  
Best Local Similarity 24.3%; Pred. No. 4.9e-12;  
RESULT 759  
ID AAG5805 standard; protein; 628 AA.  
DE Human leucine-rich repeat (LRR) family member, 33395 polypeptide.  
PN WO200172827-A2.  
PD 04-OCT-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.3%; Score 324; DB 4; Length 628;  
Best Local Similarity 24.1%; Pred. No. 4.9e-12;  
RESULT 760  
ID ADN95165 standard; protein; 810 AA.  
DE Human BEC/LEC-related protein sequence SeqID87.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 10.3%; Score 322.5; DB 7; Length 810;  
Best Local Similarity 22.0%; Pred. No. 8.2e-12;  
RESULT 761  
ID ABR58642 standard; protein; 811 AA.  
DE Human cancer related protein SEQ ID NO:299.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.3%; Score 322.5; DB 6; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.3e-12;  
RESULT 762  
ID AAO23114 standard; protein; 811 AA.  
DE KIAA0644 'human modifier of p53 pathway' protein.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.3%; Score 322.5; DB 6; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.3e-12;  
RESULT 763  
ID ADN95110 standard; protein; 811 AA.  
DE Human LEC protein sequence SeqID32.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 10.3%; Score 322.5; DB 7; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.3e-12;  
RESULT 764  
ID ADQ21196 standard; protein; 811 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.3%; Score 322.5; DB 8; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.3e-12;  
RESULT 765  
ID ADR45590 standard; protein; 605 AA.  
DE Homologue of LRSG-1, baboon ALS.  
PN US2004176296-A1.  
PD 09-SEP-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.3%; Score 322; DB 8; Length 605;  
Best Local Similarity 36.2%; Pred. No. 6.3e-12;  
RESULT 766  
ID AAG67523 standard; protein; 628 AA.  
DE Amino acid sequence of a human secreted polypeptide.  
PN WO200166690-A2.  
PD 13-SEP-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 10.2%; Score 321; DB 4; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 767  
ID AAB84469 standard; protein; 628 AA.  
DE Amino acid sequence of an interferon omega-1 like protein NOV2.  
PN WO200142471-A2.  
PD 14-JUN-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.2%; Score 321; DB 4; Length 628;

Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 768  
ID ABP69326 standard; protein; 628 AA.  
DE Human polypeptide SEQ ID NO 1373.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.2%; Score 321; DB 5; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 769  
ID ADF69107 standard; protein; 628 AA.  
DE Human MP53 protein sequence SEQ ID NO:77.  
PN WO2003083047-A2.  
PD 09-OCT-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.2%; Score 321; DB 7; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 770  
ID ADH71652 standard; protein; 628 AA.  
DE Human protein of the invention NOV22a SEQ ID NO:548.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 771  
ID ADH71654 standard; protein; 628 AA.  
DE Human protein of the invention NOV22b SEQ ID NO:550.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 772  
ID ABO84502 standard; protein; 628 AA.  
DE Human cancer-associated protein HP14-035.3.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 773  
ID ABO84503 standard; protein; 628 AA.  
DE Human cancer-associated protein HP14-035.4.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 774  
ID ABO84501 standard; protein; 628 AA.  
DE Human cancer-associated protein HP14-035.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 7.6e-12;  
RESULT 775  
ID ABP70928 standard; protein; 762 AA.  
DE Human LP341 protein.  
PN WO2003029778-A2.  
PD 10-APR-2003.  
PA (ELLIL) LILLY & CO ELI.  
Query Match 10.2%; Score 321; DB 6; Length 762;  
Best Local Similarity 25.5%; Pred. No. 9.6e-12;  
RESULT 776  
ID ADI36917 standard; protein; 797 AA.  
DE Human LRR protein #12.  
PN US2003220263-A1.  
PD 27-NOV-2003.  
PA (FEDE/) FEDER J N.  
PD (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.

Query Match 10.2%; Score 321; DB 8; Length 797;  
Best Local Similarity 25.5%; Pred. No. 1e-11;  
RESULT 777  
ID ADS98018 standard; protein; 803 AA.  
DE Protein factor discovery related isolated human polypeptide, SEQ ID 282.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA/) DRMANAC R T.  
Query Match 10.2%; Score 321; DB 8; Length 803;  
Best Local Similarity 25.5%; Pred. No. 1e-11;  
RESULT 778  
ID AAY13349 standard; protein; 660 AA.  
DE Amino acid sequence of protein PRO265.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 2; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 779  
ID ADC78348 standard; protein; 660 AA.  
DE Human PRO265 protein.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 3; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 780  
ID AAB80217 standard; protein; 660 AA.  
DE Human PRO265 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 781  
ID AAB31208 standard; protein; 660 AA.  
DE Amino acid sequence of human polypeptide PRO265.  
PN WO200077037-A2.  
PD 21-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 782  
ID AAU12346 standard; protein; 660 AA.  
DE Human PRO265 polypeptide sequence.  
PN WO200104046-A2.  
PD 07-JUN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 783  
ID ABB84839 standard; protein; 660 AA.  
DE Human PRO265 protein sequence SEQ ID NO:46.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 5; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 784  
ID ABB95445 standard; protein; 660 AA.  
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M B.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 10.2%; Score 320; DB 5; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 785  
ID ABU71595 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2002146709-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 786  
ID ABO17790 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 787  
ID ABU71450 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 788  
ID ABO25179 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 789  
ID ABU81044 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 790  
ID ABU71896 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 791  
ID ABO01779 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 792  
ID ABU66744 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 793  
ID ABU54352 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 794  
ID ABU67297 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 795  
ID AAO23116 standard; protein; 660 AA.  
DE FLRT2 'human modifier of p53 pathway' protein.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 796  
ID ABO47367 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 797  
ID ABUS9825 standard; protein; 660 AA.  
DE Novel secreted and transmembrane protein PRO265.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 798  
ID ABO25015 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein (PRO) #175.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 799  
ID ABU64504 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 800  
ID ABU72065 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US200217165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 801  
ID ABU67350 standard; protein; 660 AA.  
DE Human secreted protein PRO265.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 802

ID	ABU67166 standard; protein; 660 AA.
DE	Novel human secreted and transmembrane protein PRO265.
PN	US2003032062-A1.
PD	13-FEB-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 803	
ID	ABO14870 standard; protein; 660 AA.
DE	Human secreted / transmembrane polypeptide PRO265.
PN	US2003036060-A1.
PD	20-FEB-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 804	
ID	ABU67020 standard; protein; 660 AA.
DE	Human secreted/transmembrane, PRO, protein SEQ ID 350.
PN	US2003032155-A1.
PD	13-FEB-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 805	
ID	ABU69627 standard; protein; 660 AA.
DE	Novel human secreted and transmembrane protein PRO265.
PN	US2003017463-A1.
PD	23-JAN-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 806	
ID	ABU79808 standard; protein; 660 AA.
DE	Human secreted/transmembrane protein PRO265.
PN	US2003032057-A1.
PD	13-FEB-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 807	
ID	ABO14809 standard; protein; 660 AA.
DE	Human secreted / transmembrane polypeptide PRO265.
PN	US2003027143-A1.
PD	06-FEB-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 808	
ID	ADA45869 standard; protein; 660 AA.
DE	Novel human secreted and transmembrane protein PRO265.
PN	US2003022328-A1.
PD	30-JAN-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 809	
ID	ADA76300 standard; protein; 660 AA.
DE	Human PRO polypeptide #175.
PN	US2003073212-A1.
PD	17-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 810	
ID	ADB29233 standard; protein; 660 AA.
DE	Human secreted/transmembrane protein, #7.
PN	US2003092002-A1.
PD	15-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 811	
ID	ADA18950 standard; protein; 660 AA.
DE	Human PRO polypeptide #175.
PN	US2003073215-A1.
PD	17-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 812	
ID	ADA61573 standard; protein; 660 AA.
DE	Homo sapiens.
PN	US2003049816-A1.
PD	13-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 813	
ID	ADB19358 standard; protein; 660 AA.
DE	Novel human secreted and transmembrane protein PRO265.
PN	US2003086796-A1.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 814	
ID	ADB27899 standard; protein; 660 AA.
DE	Human PRO polypeptide #175.
PN	US2003082704-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 815	
ID	ADA86378 standard; protein; 660 AA.
DE	Novel human secreted and transmembrane protein PRO265.
PN	US2003082711-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 816	
ID	ADB15942 standard; protein; 660 AA.
DE	Human PRO polypeptide #175.
PN	US2003087350-A1.
PD	08-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 817	
ID	ADA47728 standard; protein; 660 AA.
DE	Human PRO polypeptide #175.
PN	US2003073215-A1.
PD	17-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 818	
ID	ADA18089 standard; protein; 660 AA.
DE	Human secreted/transmembrane protein, #7.
PN	US2003039971-A1.
PD	27-FEB-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 819	
ID	ABO32761 standard; protein; 660 AA.
DE	Human secreted/transmembrane protein PRO265.
PN	US2003045693-A1.
PD	06-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	10.2%; Score 320; DB 6; Length 660;
Best Local Similarity	22.4%; Pred. No. 9.3e-12;
RESULT 820	
ID</	

PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 821  
ID ADB30530 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 822  
ID ADA85826 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 823  
ID ADA97038 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 824  
ID ADA79342 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 825  
ID ADA87481 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 826  
ID ADB16683 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 827  
ID ABO34821 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 828  
ID ADA16064 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 829  
ID ADA91775 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082694-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 830  
ID ADB14838 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 831  
ID ADA47287 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 832  
ID ADB18799 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 833  
ID ADA94014 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 834  
ID ADB19910 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 835  
ID ADB13222 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 836  
ID ABO43323 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 837  
ID ADA74476 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 838  
ID ADA42209 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054401-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 839  
ID ADA6973 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US200307713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 840  
ID ADA8233 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 841  
ID ADA75196 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 842  
ID ADA85274 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 843  
ID ADA84722 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 844  
ID ABO17499 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 845  
ID ADB23978 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 846  
ID ADA80506 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 847  
ID ADA75748 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 848  
ID ADA6973 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 849  
ID ADB25269 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US200307715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 850  
ID ADA93445 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US200307721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 851  
ID ADB26795 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 852  
ID ADB31082 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 853  
ID ADA61010 standard; protein; 660 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 854  
ID ADB24157 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US200307714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 855  
ID ADA96486 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 856  
ID ADA81058 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 857  
ID ADA75748 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;

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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 857
ID ADA95934 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 858
ID ADB26243 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 859
ID ADB21728 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 860
ID ADA77507 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 861
ID ADB18247 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 862
ID ADA86930 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 863
ID ADA16488 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 864
ID ADA12917 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 865
ID ADA41785 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
|
RESULT 866
ID ADA88033 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 867
ID ADA46421 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 868
ID ADA17132 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 869
ID ADA42635 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 870
ID ADB28451 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 871
ID ADB29003 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 872
ID ADA76955 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 873
ID ADA88585 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 874
ID ADA97590 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082886-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 875
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ID ADB27347 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 876  
ID ADB22280 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 877  
ID ABO19866 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 878  
ID ABO17560 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 879  
ID ADA66971 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 880  
ID ADB22832 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 881  
ID ADB23605 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 882  
ID ADA92327 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 883  
ID ADB15390 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 884  
ID ADB38642 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 885  
ID ADB38090 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 886  
ID ADB66562 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 887  
ID ADB89642 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 888  
ID ADB90374 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 889  
ID ADB77554 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 890  
ID ADB39475 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 891  
ID ADB74690 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 892  
ID ADB47098 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 893  
ID ADB86705 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 894  
ID ADB86705 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082697-A1.  
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 894
ID ADB77310 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 895
ID ADB34467 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077117-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 896
ID ADB35571 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077119-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 897
ID ADB33915 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077116-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 898
ID ADB35019 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077118-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 899
ID ADB36123 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 900
ID ADB46518 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO365.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 901
ID ADC28336 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 902
ID ADC39536 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 903
ID ADC40050 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 904
ID ADC18878 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 905
ID ADC34174 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 906
ID ADC29229 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 907
ID ADC28760 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 908
ID ADC40645 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 909
ID ADC19302 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 910
ID ADC33750 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 911
ID ADC12820 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 912  
ID ADC50391 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 913  
ID ADC71938 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 914  
ID ADC59917 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 915  
ID ADC52924 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 916  
ID ADC57278 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 917  
ID ADC50469 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 918  
ID ADC50944 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 919  
ID ADC65471 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 920  
ID ADC54569 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 921  
ID ADC53530 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 922  
ID ADC59053 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 923  
ID ADC55931 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 924  
ID ADC58501 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein Seq ID350.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 925  
ID ADC12272 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 926  
ID ADD03175 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 927  
ID ADC90167 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 928  
ID ADC69586 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 929  
ID ADC48475 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 930  
ID ADC48475 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 930

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ID ADD10004 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 931
ID ADD04579 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 932
ID ADC080535 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 933
ID ADD11042 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 934
ID ADD10335 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 935
ID ADC47923 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 936
ID ADD04827 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 937
ID ADC79983 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 938
ID ADD11295 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 939
ID ADD09452 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 940
ID ADD03833 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 941
ID ADD03409 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 942
ID ADD41165 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 943
ID ADD52304 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 944
ID ADD53044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 945
ID ADD53596 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 946
ID ADD37088 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 947
ID ADD51752 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 948
ID ADD02551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
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PD US2003203431-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 949  
ID ADD01985 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 950  
ID ADD54167 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 951  
ID ADD92484 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 952  
ID ADD91380 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199035-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 953  
ID ADE03994 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 954  
ID ADE32291 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 955  
ID ADE22223 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 956  
ID ADD79447 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 957  
ID ADE41983 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194772-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 958  
ID ADE17800 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 959  
ID ADD91932 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 960  
ID ADE33395 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 961  
ID ADE33947 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 962  
ID ADD79999 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 963  
ID ADD93036 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 964  
ID ADE19456 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 965  
ID ADE34661 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 966  
ID ADE18904 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199026-A1.  
PD 23-OCT-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 967
ID ADE43100 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 968
ID ADD95889 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 969
ID ADE22775 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 970
ID ADD78893 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 971
ID ADE32843 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194786-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 972
ID ADE42535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 973
ID ADD80551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 974
ID ADD89579 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 975
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 976
ID ADE04662 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 977
ID ADE92791 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 978
ID ADG21500 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 979
ID ADG23141 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 980
ID ADF97476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 981
ID ADG80540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 982
ID ADG79988 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 983
ID ADG63796 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 984
ID ADH59144 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 985
ID ADH55280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 986
ID ADH55832 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 987
ID ADI37923 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 988
ID ADI65000 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 989
ID ADI63499 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 990
ID ADH81913 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 991
ID ADH81361 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 992
ID ADJ26191 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 993
ID ADM82530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 994
ID ADNI5929 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 995
ID ADNI6558 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 996
ID ADNI5377 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 997
ID ADNI4825 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 998
ID ADI64051 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 999
ID ADC81087 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1000
ID ADE79106 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1001
ID ADD76535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1002
ID ADD87899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1003
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ID ADE96303 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1004
ID ADE9530 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1005
ID ADE75751 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1006
ID ADE73206 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1007
ID ADE41296 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1008
ID ADE23327 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1009
ID ADE23879 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1010
ID ADE24522 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1011
ID ADE87347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1012
ID ADE99213 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1013
ID ADE41210 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1014
ID ADE73741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1015
ID ADE18352 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1016
ID ADE88661 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US200319054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1017
ID ADE99295 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1018
ID ADE94681 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1019
ID ADE91092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1020
ID ADE95233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1021
ID ADE93343 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
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PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1022  
ID ADF34924 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1023  
ID ADE98414 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1024  
ID ADE92239 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1025  
ID ADE90540 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1026  
ID ADE91687 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1027  
ID ADE98841 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1028  
ID ADG40311 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1029  
ID ADF73705 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1030  
ID ADG02266 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1031  
ID ADG22052 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO365.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1032  
ID ADG20122 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1033  
ID ADF98028 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1034  
ID ADG34245 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO365.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1035  
ID ADF98599 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1036  
ID ADG03430 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1037  
ID ADF99151 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1038  
ID ADG16736 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;

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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1039
ID ADG05195 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1040
ID ADG19462 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1041
ID ADF73281 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003186051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1042
ID ADG13299 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1043
ID ADG08356 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1044
ID ADG15526 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1045
ID ADF96924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1046
ID ADG06109 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1047
ID ADG23693 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1048
ID ADG03982 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1049
ID ADG24883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1050
ID ADG07180 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1051
ID ADG07732 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1052
ID ADG55227 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1053
ID ADG60891 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1054
ID ADG61995 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1055
ID ADG92124 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1056
ID ADG82196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1057
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ID ADG57435 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1058  
ID ADG56883 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1059  
ID ADG55779 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1060  
ID ADG58539 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1061  
ID ADG70905 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1062  
ID ADG92551 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1063  
ID ADG57987 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1064  
ID ADG53571 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1065  
ID ADG71457 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1066  
ID ADG81644 standard; protein; 660 AA.

DE Human PRO polypeptide #175.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1067  
ID ADH30606 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1068  
ID ADG63645 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1069  
ID ADH11973 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1070  
ID ADG52395 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1071  
ID ADG54123 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1072  
ID ADG81092 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1073  
ID ADG56331 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1074  
ID ADH12597 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1075  
ID ADG61443 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207429-A1.

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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1076
ID ADH28530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1077
ID ADG54675 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1078
ID ADG59715 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1079
ID ADH20340 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1080
ID ADH3479 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1081
ID ADH07195 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1082
ID ADH59740 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1083
ID ADH06768 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1084
ID ADI81139 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1085
ID ADI18510 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1086
ID ADI65230 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1087
ID ADI37493 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1088
ID ADG09882 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1089
ID ADH97297 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1090
ID ADI15353 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1091
ID ADG09230 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1092
ID ADI14685 standard; protein; 660 AA.
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DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1093  
ID ADH60400 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHIER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1094  
ID ADI18280 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1095  
ID ADJ99457 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1096  
ID ADL08650 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1097  
ID ADM24995 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1098  
ID ADJ63561 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1099  
ID ADM29741 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1100  
ID ADJ77456 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004038336-A1.  
PD 26-FEB-2004.

PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1101  
ID ADK82824 standard; protein; 660 AA.  
DE Human PRO polypeptide #23.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1102  
ID ADJ65578 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1103  
ID ADM27714 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1104  
ID ADM24238 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1105  
ID ADO06063 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1106  
ID ADM28300 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1107  
ID ADR10915 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.3e-12;  
RESULT 1108  
ID ADR17824 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.

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PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1109
ID ADI95782 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077659-A1
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1110
ID ADI96334 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1111
ID ADI65657 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1112
ID ADS74463 standard; protein; 660 AA.
DE Human secreted/transmembrane protein #7.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1113
ID ADS32286 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1114
ID ADT03270 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1115
ID ADT03500 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1116
ID ADU06386 standard; protein; 660 AA.
DE Novel bronchial cancer-associated human protein SeqID610.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1117
ID ADZ03321 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO265 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1118
ID AEA37738 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1119
ID AEB14067 standard; protein; 660 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
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RESULT 1120  
ID ADT77808 standard; protein; 452 AA.  
DE Chimeric Nogo receptor polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 10.2%; Score 318.5; DB 8; Length 452;  
Best Local Similarity 27.3%; Pred. No. 7.5e-12;  
RESULT 1121  
ID ADT77802 standard; protein; 452 AA.  
DE Chimeric Nogo receptor polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 10.2%; Score 318.5; DB 8; Length 452;  
Best Local Similarity 27.8%; Pred. No. 7.5e-12;  
RESULT 1122  
ID AAE13006 standard; protein; 713 AA.  
DE Human leucine-rich repeat (LRR) family member protein.  
PN WO200175105-A2.  
PD 11-OCT-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 317.5; DB 4; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.5e-11;  
RESULT 1123  
ID AAU91335 standard; protein; 713 AA.  
DE Human novel secreted protein LP223(a).  
PN WO200214358-A2.  
PD 21-FEB-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.1%; Score 316.5; DB 5; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.7e-11;  
RESULT 1124  
ID ABG97991 standard; protein; 713 AA.  
DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.  
PN WO200274959-A2.  
PD 26-SEP-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.1%; Score 316.5; DB 5; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.7e-11;  
RESULT 1125  
ID ABUE2381 standard; protein; 713 AA.  
DE Human GPCR related protein NOV31a.  
PN WO200279398-A2.  
PD 10-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.1%; Score 316.5; DB 6; Length 713;  
Best Local Similarity 23.1%; Pred. No. 1.7e-11;  
RESULT 1126  
ID ADT77796 standard; protein; 474 AA.  
DE Chimeric Nogo receptor polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 10.0%; Score 314.5; DB 8; Length 474;  
Best Local Similarity 27.8%; Pred. No. 1.4e-11;  
RESULT 1127  
ID AAU91341 standard; protein; 656 AA.  
DE Human novel secreted protein LP223(b).  
PN WO200214358-A2.  
PD 21-FEB-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.0%; Score 313.5; DB 5; Length 656;  
Best Local Similarity 23.6%; Pred. No. 2.4e-11;  
RESULT 1128  
ID ADL24097 standard; protein; 713 AA.  
DE Human NOVX polypeptide #71.  
PN US2004002120-A1.  
PD 01-JAN-2004.  
PA (KEKU/) KEKUDA R.  
PA (TCHH/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.

PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (MALI/) MALYANKAR U M.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (CASM/) CASMAN S J.  
PA (PENA/) PENNA C E A.  
PA (GANG/) GANGOLLI E A.  
PA (GUSE/) GUSEV V Y.  
PA (SMIT/) SMITHSON G.  
PA (ZERR/) ZERHUSEN B D.  
PA (GERL/) GERLACH V.  
PA (POCH/) POCHART P F.  
PA (FERN/) FERNANDES E R.  
PA (SHIM/) SHIMKETS R A.  
PA (RAST/) RASTELLI L.  
PA (SPAD/) SPADERNA S K.  
PA (LARO/) LAROCHELLE W J.  
PA (ZHON/) ZHONG M.  
PA (KHRA/) KHRAMTSOV N V.  
PA (VOSS/) VOSS E Z.  
PA (HERR/) HERRMANN J L.  
Query Match 10.0%; Score 313.5; DB 8; Length 713;  
Best Local Similarity 23.1%; Pred. No. 2.6e-11;  
RESULT 1129  
ID AAE09437 standard; protein; 592 AA.  
DE Human ebgTango79a protein.  
PN WO200160850-A1.  
PD 23-AUG-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 10.0%; Score 312; DB 4; Length 592;  
Best Local Similarity 25.9%; Pred. No. 2.6e-11;  
RESULT 1130  
ID AAE25351 standard; protein; 592 AA.  
DE Human LP polypeptide, LP243.  
PN WO200248361-A2.  
PD 20-JUN-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.0%; Score 312; DB 5; Length 592;  
Best Local Similarity 25.9%; Pred. No. 2.6e-11;  
RESULT 1131  
ID AAU91329 standard; protein; 592 AA.  
DE Human novel secreted protein LP243(b).  
PN WO200214358-A2.  
PD 21-FEB-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.0%; Score 312; DB 5; Length 592;  
Best Local Similarity 25.9%; Pred. No. 2.6e-11;  
RESULT 1132  
ID ABP60996 standard; protein; 592 AA.  
DE Novel human protein. SEQ ID 83.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 10.0%; Score 312; DB 5; Length 592;  
Best Local Similarity 25.9%; Pred. No. 2.6e-11;  
RESULT 1133  
ID AAU79167 standard; protein; 592 AA.  
DE Human leucine-rich repeat proteins-like protein NOV4.  
PN WO200214368-A2.  
PD 21-FEB-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.0%; Score 312; DB 5; Length 592;

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Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1134
ID ABG74693 standard; protein; 592 AA.
DE Human CDD protein 6803363CD1 SEQ ID 19.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCV-) INCVTE GENOMICS INC.
Query Match 10.0%; Score 312; DB 6; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1135
ID ADE03417 standard; protein; 592 AA.
DE Human immunoglobulin superfamily member BGS-2.
PN US2003195163-A1.
PD 16-OCT-2003.
PA (WUSS/) WU S.
PA (KRYSS/) KRYSTEK S R.
PA (LEEL/) LEE L.
PA (FEDE/) FEDER J N.
PA (CHEN/) CHENG J D.
Query Match 10.0%; Score 312; DB 7; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1136
ID ADU02709 standard; protein; 592 AA.
DE Novel human polypeptide seqid 1176.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.0%; Score 312; DB 8; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1137
ID ABG61770 standard; protein; 608 AA.
DE Novel leucine-rich protein.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 312; DB 5; Length 608;
Best Local Similarity 25.9%; Pred. No. 2.7e-11;
RESULT 1138
ID ABG97967 standard; protein; 634 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 9.9%; Score 311; DB 5; Length 634;
Best Local Similarity 24.1%; Pred. No. 3.3e-11;
RESULT 1139
ID ABR55628 standard; protein; 420 AA.
DE Amino acid sequence of rat Nogo-66 receptor homologue Ngrh1.
PN WO2003035687-A1.
PD 01-MAY-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 9.9%; Score 310.5; DB 6; Length 420;
Best Local Similarity 29.8%; Pred. No. 2.2e-11;
RESULT 1140
ID ADT77788 standard; protein; 420 AA.
DE Rat Nogo receptor 2 polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
Query Match 9.9%; Score 310.5; DB 8; Length 420;
Best Local Similarity 29.8%; Pred. No. 2.2e-11;
RESULT 1141
ID AAO23115 standard; protein; 674 AA.
DE FLRT1 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 9.9%; Score 310.5; DB 6; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1142
ID ADH17606 standard; protein; 674 AA.
DE Human NOV19a protein - SEQ ID 296.
PN WO200116318-A2.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1143
ID ADH17628 standard; protein; 674 AA.
DE Human NOV19l protein - SEQ ID 318.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1144
ID ADH17630 standard; protein; 674 AA.
DE Human NOV19m protein - SEQ ID 320.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1145
ID ADH17634 standard; protein; 674 AA.
DE Human NOV19o protein - SEQ ID 324.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1146
ID ADH17632 standard; protein; 674 AA.
DE Human NOV19n protein - SEQ ID 322.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1147
ID ABO27346 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO1865.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4e-11;
RESULT 1148
ID ABO34232 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4e-11;
RESULT 1149
ID AAU29215 standard; protein; 649 AA.
DE Human PRO polypeptide sequence #192.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1150
ID AAB70533 standard; protein; 649 AA.
DE Human PRO3 protein sequence SEQ ID NO:6.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1151
ID AAB87591 standard; protein; 649 AA.
DE Human PRO1865.
PN WO200116318-A2.
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PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 4; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1152  
ID ABG95916 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein PRO1865.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1153  
ID ABB4953 standard; protein; 649 AA.  
DE Human PRO1865 protein sequence SEQ ID NO:274.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1154  
ID ABP70109 standard; protein; 649 AA.  
DE Human NOV27a.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1155  
ID ABB9559 standard; protein; 649 AA.  
DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1156  
ID ABUS8591 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1157  
ID ABUS88139 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1158  
ID ABUS84454 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1159  
ID ABR75034 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040056-A1.

ID ABR66328 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1160  
ID ABR65718 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1161  
ID ABUS9658 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1162  
ID ABUS2897 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1163  
ID ABUS90018 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1164  
ID ABR68267 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1165  
ID ABUS6320 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1166  
ID ABUS92751 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1167  
ID ABO08828 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1168  
ID ABO02880 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1169  
ID ABR75034 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040056-A1.

PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1170  
ID ABR94796 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1171  
ID ABU85769 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1172  
ID ABUS9829 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003013153-A1  
PD 16-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1173  
ID ABUS98144 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1174  
ID ABUS1850 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1175  
ID ABUS9543 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1176  
ID ABUS6384 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1177  
ID ABUS67597 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1178  
ID ABUS0625 standard; protein; 649 AA.  
DE Human PRO protein #192.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1179  
ID ABUS0941 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.

PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1180  
ID ABO34000 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein PRO1865.  
PN US200309013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1181  
ID ABR99543 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1182  
ID ABR98933 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1183  
ID ABO16456 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1184  
ID ABR92356 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1185  
ID ABO18997 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1186  
ID ABR78418 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1187  
ID ABUS72017 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1188  
ID ABUS5154 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1189  
ID ABO00293 standard; protein; 649 AA.

DE Novel human secreted and transmembrane protein PRO1865.  
FN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1190 22.3%; Pred. No. 4.6e-11;  
ID ABO11825 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1191 22.3%; Pred. No. 4.6e-11;  
ID ABO02270 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1192 22.3%; Pred. No. 4.6e-11;  
ID ABU88844 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
FN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1193 22.3%; Pred. No. 4.6e-11;  
ID ABU83539 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1194 22.3%; Pred. No. 4.6e-11;  
ID ABO06340 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
FN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1195 22.3%; Pred. No. 4.6e-11;  
ID ABR59376 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1196 22.3%; Pred. No. 4.6e-11;  
ID ABO09438 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1197 22.3%; Pred. No. 4.6e-11;  
ID ABO19302 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
FN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1198 22.3%; Pred. No. 4.6e-11;  
ID ABO11320 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1199 22.3%; Pred. No. 4.6e-11;  
ID ABR66938 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003036148-A1.

PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1200 22.3%; Pred. No. 4.6e-11;  
ID ABO16151 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1201 22.3%; Pred. No. 4.6e-11;  
ID ABO13857 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1202 22.3%; Pred. No. 4.6e-11;  
ID ABU71571 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865.  
FN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1203 22.3%; Pred. No. 4.6e-11;  
ID ABU65760 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein, SEQ ID 384.  
FN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1204 22.3%; Pred. No. 4.6e-11;  
ID ABO07608 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
FN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1205 22.3%; Pred. No. 4.6e-11;  
ID ABO03795 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1206 22.3%; Pred. No. 4.6e-11;  
ID ABR67243 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1207 22.3%; Pred. No. 4.6e-11;  
ID ABO15846 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1208 22.3%; Pred. No. 4.6e-11;  
ID ABU56127 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein, PRO1865.  
FN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1209 22.3%; Pred. No. 4.6e-11;  
ID ABU72352 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
FN US2002182638-A1.  
PD 05-DEC-2002.

PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1210  
ID ABU65455 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1211  
ID ABU95400 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1212  
ID ABU71303 standard; protein; 649 AA.  
DE Human PRO1865 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1213  
ID ABO07913 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1214  
ID ABR70154 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1215  
ID ABR69487 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1216  
ID ABO01628 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1217  
ID ABU81430 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1218  
ID ABR0227 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1219  
ID ABU91025 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2003018168-A1.  
PD 23-JAN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1220  
ID ABR67962 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1221  
ID ABR65350 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1222  
ID ABR68572 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1223  
ID ABR71984 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1224  
ID ABU85464 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1225  
ID ABU89154 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1226  
ID ABU83234 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1227  
ID ABU95090 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1228  
ID ABU90638 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1229  
ID ABU84149 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;

Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1230  
ID ABU93800 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1231  
ID ABR65045 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1232  
ID ABR68877 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1233  
ID ABO06693 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1234  
ID ABR99238 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1235  
ID ABU57122 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1236  
ID ABU86074 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1237  
ID ABU82361 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1238  
ID ABU87372 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1239  
ID ABU83644 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1240

ID ABO08218 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1241  
ID ABU92541 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein PRO1865.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1242  
ID ABU81929 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1243  
ID ABU66093 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1244  
ID ABU81211 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1245  
ID ABR59922 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1246  
ID ABU94110 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1247  
ID ABU99963 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1248  
ID ABR66633 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1249  
ID ABR91051 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1250

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ID ABO53325 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1251
ID ABU94478 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017540-A1.
PD 23-JAN-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1252
ID ABU79360 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032106-A1.
PD 13-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1253
ID ABU86689 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032129-A1.
PD 13-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1254
ID ABU86994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032131-A1.
PD 13-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1255
ID ABU94783 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032103-A1.
PD 13-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1256
ID ABO04710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032107-A1.
PD 13-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1257
ID ABR70459 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032139-A1.
PD 13-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1258
ID ABU98624 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022301-A1.
PD 30-JAN-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1259
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1260
ID ABR64740 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022293-A1.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027262-A1.
PD 06-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1261
ID ABU79665 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032110-A1.
PD 13-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1262
ID ABU93056 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036142-A1.
PD 20-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1263
ID ABU96015 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036145-A1.
PD 20-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1264
ID ABU91235 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036154-A1.
PD 20-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1265
ID ABU90328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036153-A1.
PD 20-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1266
ID ABO09743 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044931-A1.
PD 06-MAR-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1267
ID ABO11015 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036150-A1.
PD 20-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1268
ID ABR71069 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040069-A1.
PD 27-FEB-2003.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1269
ID ABU98328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match      9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1270
ID ABU87677 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022293-A1.
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PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1271  
ID ABU91545 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1272  
ID ABU89333 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1273  
ID ABU84759 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1274  
ID ABR69849 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1275  
ID ABU80226 standard; protein; 649 AA.  
DE Human PRO protein #192.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1276  
ID ABU82540 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1277  
ID ABU93495 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1278  
ID ABO10048 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1279  
ID ABO09133 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1280  
ID ABU96504 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2003027993-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1281  
ID ABU10701 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein #192.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1282  
ID ABU72174 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1283  
ID ABU95710 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1284  
ID ABU96919 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1285  
ID ABR70764 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1286  
ID ABO05115 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1287  
ID ABO08523 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1288  
ID ABO05730 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1289  
ID ABR74119 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1290  
ID ABR95711 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1291  
ID ABR81008 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1292  
ID ABR81313 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1293  
ID ABR88611 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1294  
ID ABR77432 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1295  
ID ABR77432 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1296  
ID ABO28916 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1297  
ID ABO31661 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1298  
ID ABO08078 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1299  
ID ABO40558 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068682-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1300  
ID ABO35983 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1301  
ID ABO44122 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1302  
ID ADA78136 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1303  
ID ABM24917 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1304  
ID ABO03185 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1305  
ID ABR90441 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1306  
ID ABM17355 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1307  
ID ABR95101 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1308  
ID ABR95406 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1309

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ID ADB17189 standard; protein; 649 AA.
DE Human transmembrane PRO polypeptide (SeqID 132).
PD US2003050462-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1310
ID ABO211644 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PD US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1311
ID ABR97908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1312
ID ABR87696 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1313
ID ABM77737 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1314
ID ABM27967 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1315
ID ABM6248 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1316
ID ABM03754 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1317
ID ABM35205 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1318
ID ABM26442 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003068699-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1319
ID ABO48224 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PD US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1320
ID ABR92966 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1321
ID ABO24727 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PD US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1322
ID ABM11738 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1323
ID ABM02839 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1324
ID ABM16135 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1325
ID ABO27696 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PD US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1326
ID ABM29187 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1327
ID ABM07163 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PD US2003068699-A1.
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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1328
ID ABM21257 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1329
ID ABM09603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1330
ID ABO41473 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1331
ID ABO36288 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1332
ID ABO43817 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1333
ID ABM76517 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1334
ID ABM76213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1335
ID ABM25832 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1336
ID ABM26137 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1337
ID ABO03490 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1338
ID ABO02575 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1339
ID ABO44304 standard; protein; 649 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1340
ID ABR90746 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1341
ID ABR73814 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1342
ID ABO17066 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1343
ID ABR94491 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1344
ID ABR75998 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1345
ID ABR71374 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1346
ID ABR93271 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1347  
ID ABR93576 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1348  
ID ABR88001 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1349  
ID ABO28001 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1350  
ID ABO30136 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1351  
ID ABO33345 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
FN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1352  
ID ABO50503 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1353  
ID ABO808993 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1354  
ID ABO36593 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1355  
ID ABO35678 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
FN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

ID ABR87086 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1366  
ID ABM1128 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1367  
ID ABM28272 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1368  
ID ABO32271 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1369  
ID ABM15398 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1370  
ID ABM06553 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1371  
ID ABM04364 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1372  
ID ABM22477 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1373  
ID ABM07773 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1374  
ID ABO40863 standard; protein; 649 AA.

DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1375  
ID ABM35510 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1376  
ID ABM33273 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1377  
ID ABO52799 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1378  
ID ABO50359 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1379  
ID ABU99353 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1380  
ID ABO04405 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1381  
ID ABO06035 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1382  
ID ABM18575 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1383  
ID ABR97603 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;



Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1403  
PN US2003096359-A1.  
ID ABO29221 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1404  
PN US2003068735-A1.  
ID ABM24002 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1405  
PN US2003068753-A1.  
ID ABM23392 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1406  
PN US2003068756-A1.  
ID ABO37813 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1407  
PN US2003068756-A1.  
ID ABO37813 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1408  
PN US2003082715-A1.  
ID ABM28577 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1409  
PN US2003082716-A1.  
ID ABM28882 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1410  
PN US2003068737-A1.  
ID ABM66526 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1411  
PN US2003104547-A1.  
ID ABM75908 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1412  
PN US2003073172-A1.

ID ABM34188 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1413  
PN US2003100061-A1.  
ID ABM34493 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1414  
PN US2003032125-A1.  
ID ABO20424 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1415  
PN US2003054454-A1.  
ID ABO21339 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1416  
PN US2003054477-A1.  
ID ABO22254 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1417  
PN US2003055222-A1.  
ID ADA20166 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1418  
PN US2003054460-A1.  
ID ABR96688 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1419  
PN US2003049753-A1.  
ID ABR5866 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1420  
PN US2003049763-A1.  
ID ABR99848 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
RESULT 1421  
PN US2003073172-A1.  
ID ABM00399 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073172-A1.

PD 17-APR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1422  
ID ABM00704 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1423  
ID ABO29831 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1424  
ID ABM23697 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1425  
ID ABM29492 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1426  
ID ABO38423 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1427  
ID ABO45723 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1428  
ID ABM20647 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1429  
ID ADA81655 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1430  
ID ABO16761 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1431  
ID ABO18387 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1432  
ID ABO22814 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1433  
ID ABO23119 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1434  
ID ABR92661 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1435  
ID ABR81618 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1436  
ID ABM78042 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1437  
ID ABR89831 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1438  
ID ABM26747 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1439  
ID ABM13873 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1440  
ID ABO28611 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064460-A1.  
PD 03-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1441
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1442
ID ABO51579 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1443
ID ABO4059 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1444
ID ABO37203 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1445
ID ABO41778 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1446
ID ABO35373 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1447
ID ABM25222 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1448
ID ABO47614 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1449
ID ABO47919 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1450
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1451
ID ABO51579 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1452
ID ABO51884 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1453
ID ABO50664 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1454
ID ABR79788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1455
ID ABM17050 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1456
ID ABO18082 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1457
ID ABO21034 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1458
ID ABR96993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1459
ID ABM12348 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
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PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1479  
ID ABR76603 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1480  
ID ABR73204 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1481  
ID ABM18270 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1482  
ID ABO20729 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1483  
ID ABO25472 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1484  
ID ABO25777 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1485  
ID ABR94186 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1486  
ID ABR80093 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1487  
ID ABM11433 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1488  
ID ABO33040 standard; protein; 649 AA.

DE Human PRO polypeptide #192.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1489  
ID ABO30746 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1490  
ID ABO31051 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1491  
ID ABM27357 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1492  
ID ABM30102 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1493  
ID ABM05638 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1494  
ID ABM15703 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1495  
ID ABM08688 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1496  
ID ABO42388 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1497  
ID ABO38118 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.

PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1498  
ID ABO46028 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1499  
ID AEM66831 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;  
RESULT 1500  
ID ADB20496 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

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103	148.5	4.7	890	2	C96654	hypothetical prote	176	136	4.3	4957	2	T03455	ALR protein - huma
104	148.5	4.7	964	2	T49038	hypothetical prote	177	135.5	4.3	427	2	JC4915	ags protein precu
105	148.5	4.7	1115	2	S40241	G protein-coupled	178	135.5	4.3	499	2	D83333	hypothetical prote
106	148	4.7	338	2	S52284	lumicon, secretory	179	135.5	4.3	1124	2	B84742	probable receptor-
107	148	4.7	1188	2	S49915	extensin-like prot	180	135.5	4.3	5262	2	T03454	SH3 domain binding
108	147.5	4.7	316	2	A41781	proteoglycan-Ib -	181	135	4.3	601	2	S56144	ALR protein - huma
109	147.5	4.7	1385	2	T13887	tlr protein - frui	182	134.5	4.3	613	2	T15489	hypothetical prote
110	147	4.7	1964	2	T09059	notch4 - mouse	183	134.5	4.3	847	2	F96531	hypothetical prote
111	147	4.7	2414	2	A54277	transcription adap	184	134.5	4.3	1039	2	T22117	hypothetical prote
112	146.5	4.7	382	2	T04260	hypothetical prote	185	134	4.3	530	2	A45690	transactivator EBN
113	146.5	4.7	925	2	C84538	probable LRR recep	186	134	4.3	656	2	B47096	hy1B homolog - Str
114	146.5	4.7	1408	2	S16148	gene serrate prote	187	134	4.3	886	2	T40734	probable adenylate
115	146	4.7	369	2	G83434	translocation prot	188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
116	145.5	4.6	380	2	S71876	fibromodulin - chi	189	133.5	4.3	384	2	A41710	promastigote surfa
117	145.5	4.6	886	2	S28605	glycoprotein 350/2	190	133.5	4.3	1068	2	H96769	hypothetical prote
118	145.5	4.6	2142	2	B35098	MHC class III hist	191	133	4.2	576	2	T36729	probable serine/ch
119	145	4.6	458	2	T19941	hypothetical prote	192	133	4.2	852	2	I51259	tyrosine kinase C
120	145	4.6	679	2	T20713	hypothetical prote	193	133	4.2	932	2	T48489	receptor-like prot
121	145	4.6	694	2	JC2237	foliitropin recept	194	133	4.2	1257	2	A88536	protein B0523.5 [i
122	145	4.6	1839	1	OVBVK	adenylate cyclase	195	133	4.2	4391	2	A38096	perlecan precursor
123	144.5	4.6	186	2	B84660	hypothetical prote	196	132.5	4.2	463	1	A36479	milk fat globule m
124	144.5	4.6	2187	2	T03826	nascent polypeptid	197	132.5	4.2	2035	2	A40718	host cell factor C
125	144.5	4.6	3149	1	Q0BE8	BPLFI protein - hu	198	132	4.2	3164	1	WMBEH6	UL36 protein - hum
126	144	4.6	695	2	I45896	follicle stimulat	199	131.5	4.2	346	2	T46916	hypothetical prote
127	144	4.6	1019	2	C96519	probable disease r	200	131.5	4.2	890	2	T00800	disease resistance
128	144	4.6	3020	2	A43932	mucin 2 precursor,	201	131.5	4.2	1097	2	A29943	Toll protein precu
129	143.5	4.6	243	2	B41710	promastigote surfa	202	131.5	4.2	1286	2	A88396	protein M01E0.2 [
130	143.5	4.6	476	2	T27051	hypothetical prote	203	131	4.2	612	2	T10727	protein kinase Xa2
131	143.5	4.6	496	2	C96832	hypothetical prote	204	131	4.2	767	2	B84594	probable LRR recep
132	143.5	4.6	605	2	T50817	protein serine/thr	205	131	4.2	905	2	T00475	probable disease r
133	143.5	4.6	683	2	T24486	hypothetical prote	206	131	4.2	915	2	T09575	smoothelin - human
134	142.5	4.5	1870	2	S37671	MHC class III hist	207	131	4.2	1095	2	C96746	hypothetical prote
135	142.5	4.5	1872	2	S36152	MHC class III hist	208	131	4.2	1196	2	T09356	brassinosteroid-in
136	142	4.5	661	2	I56258	RP105 - mouse	209	130.5	4.2	448	2	T27395	hypothetical prote
137	142	4.5	983	2	G84524	probable disease r	210	130	4.1	268	2	T19697	hypothetical prote
138	141.5	4.5	462	2	D84858	hypothetical prote	211	130	4.1	389	2	H86266	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote	212	130	4.1	395	2	H75457	hypothetical prote
140	141.5	4.5	1029	2	T05050	protein kinase hom	213	130	4.1	768	2	T17462	disease resistance
141	141.5	4.5	1051	2	T13174	gp150 protein - fr	214	130	4.1	800	2	H84740	hypothetical prote
142	141	4.5	630	2	AC1129	Internalin B [limp	215	129.5	4.1	315	2	T06806	proline rich prote
143	141	4.5	717	2	T33295	hypothetical prote	216	129.5	4.1	780	2	T00366	hypothetical prote
144	140.5	4.5	376	2	S55275	fibromodulin precu	217	129.5	4.1	861	2	A48825	Notch homolog Motc
145	140	4.5	277	2	I60122	rsu-1 homolog - hu	218	129.5	4.1	912	2	A54423	brevican precursor
146	140	4.5	474	2	S65763	chitinase (EC 3.2.	219	129.5	4.1	942	2	S23251	protein-tyrosine k
147	140	4.5	754	2	A85043	probable LRR recep	220	129.5	4.1	1173	2	I50620	proCK2 - chicken
148	140	4.5	1029	2	T00712	protein kinase hom	221	129.5	4.1	1469	2	T09219	basal transcriptio
149	139.5	4.4	333	2	T34555	hypothetical prote	222	129	4.1	371	2	S20075	promastigote surfa
150	139.5	4.4	527	2	A75399	hypothetical prote	223	129	4.1	835	2	T05259	probable disease r
151	139.5	4.4	539	2	G70520	probable csp prote	224	129	4.1	910	2	B96770	hypothetical prote
152	139.5	4.4	4351	2	T00252	MEGF1 protein - ra	225	129	4.1	1027	2	B85089	receptor protein k
153	139	4.4	581	2	A45551	insect-stage-speci	226	129	4.1	1064	2	B86465	probable Protein k
154	139	4.4	603	2	T24315	hypothetical prote	227	129	4.1	1232	2	T05322	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote	228	129	4.1	1329	2	A64828	cell division prot
156	139	4.4	1088	2	E86312	F11A6.9 protein -	229	129	4.1	1342	2	E85614	cell division prot
157	139	4.4	2240	2	T37057	probable multi-dom	230	129	4.1	1342	2	G90750	cell division prot
158	138.5	4.4	342	2	A46743	lumican precursor	231	129	4.1	1959	1	AGRT	agrin - rat
159	138.5	4.4	990	2	T14756	hypothetical prote	232	129	4.1	2321	2	S78549	notch3 protein - h
160	138.5	4.4	1650	2	S53457	dominant autoantig	233	128.5	4.1	4877	2	S42442	nuclear protein EB
161	138	4.4	630	2	C39930	hypothetical prote	234	128.5	4.1	677	2	H86208	protein F22G5.26 [
162	138	4.4	858	2	T00258	hypothetical prote	235	128.5	4.1	727	2	C84534	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote	236	128.5	4.1	744	2	C84527	probable receptor-
164	137.5	4.4	1151	2	T18535	high molecular mas	237	128.5	4.1	825	2	T29634	hypothetical prote
165	137.5	4.4	4860	2	T42737	gp330 protein prec	238	128.5	4.1	1113	2	T00271	hypothetical prote
166	137	4.4	562	2	T34319	hypothetical prote	239	128.5	4.1	3968	2	A44265	trithorax homolog
167	137	4.4	695	2	JC1493	foliitropin recept	240	128	4.1	597	2	S72468	probable transcrip
168	137	4.4	788	2	AG0786	secreted effector	241	128	4.1	967	2	T48210	hypothetical prote
169	137	4.4	907	1	Q0BE21	membrane antigen g	242	128	4.1	1428	2	T08852	lustrin A - Califo
170	137	4.4	4544	1	S23392	alpha-2-macroglobu	243	128	4.1	1914	2	T42635	tenascin Y precurs
171	137	4.4	4544	1	S25111	alpha-2-macroglobu	244	127.5	4.1	1750	2	D86245	hypothetical prote
172	136	4.3	322	2	S72271	proteoglycan lb pr	245	127.5	4.1	1120	2	B86479	hypothetical prote
173	136	4.3	626	2	AE0123	probable antigenic	246	127.5	4.1	1784	2	C96615	hypothetical prote
174	136	4.3	692	2	A34548	foliitropin recept	247	127	4.1	327	2	S20074	promastigote surfa
175	136	4.3	1008	2	D84434	probable receptor-	248	127	4.1	773	2	T00502	probable receptor-

249	127	4.1	775	1	EDBE11	immediate-early pr	322	121.5	3.9	432	2	E967112	unknown protein, 6
250	127	4.1	800	2	G84740	hypothetical prote	323	121.5	3.9	519	2	T07026	ethylene receptor
251	127	4.1	1366	2	T35985	probable large Pro	324	121.5	3.9	635	2	T07794	Delta-4 protein -
252	127	4.1	1895	2	T06609	disease resistance	325	121.5	3.9	686	2	JC7569	probable Pco kinas
253	127	4.1	1955	1	AGCH	agrin precursor -	326	121.5	3.9	760	2	F86387	hypothetical prote
254	126.5	4.0	288	2	T45616	hypothetical prote	327	121.5	3.9	902	2	T00588	latent transactivi
255	126.5	4.0	685	2	JC7570	Delta-4 protein -	328	121.5	3.9	1251	2	A57293	presynaptic activi
256	126.5	4.0	694	2	JC4301	follitropin recept	329	121.5	3.9	1409	2	T37188	fibronectin - bovi
257	126.5	4.0	862	2	T46289	hypothetical prote	330	121.5	3.9	2265	1	FNBO	polyketide synthas
258	126.5	4.0	999	1	S27556	receptor-like prot	331	121.5	3.9	2297	2	T34918	notch 3 protein -
259	126.5	4.0	1091	2	S33596	protein-tyrosine k	332	121.5	3.9	2318	2	S45306	unconventional myo
260	126.5	4.0	1777	2	T33369	hypothetical prote	333	121.5	3.9	3330	2	A59266	cell wall-plasma m
261	126	4.0	500	2	S49302	AWJ218 protein -	334	121	3.9	306	2	T52340	probable disease r
262	126	4.0	865	2	A47282	calcium-binding pr	335	121	3.9	480	2	T00971	sulfated surface g
263	126	4.0	873	2	A47283	calphotin - fruit	336	121	3.9	485	2	A33647	microtubule-associ
264	126	4.0	996	2	F86410	protein F3W18.12 [	337	121	3.9	733	2	A45301	Notch B protein -
265	126	4.0	1152	2	T31911	hypothetical prote	338	121	3.9	1203	2	A49175	hypothetical prote
266	126	4.0	1820	2	A55494	latent transformin	339	121	3.9	1520	2	T00273	notch protein homo
267	125.5	4.0	283	2	S13383	hydroxyproline-ric	340	121	3.9	2531	2	S18188	osteoinductive fac
268	125.5	4.0	548	2	AH1107	internalin H (impo	341	120.5	3.8	299	2	A35272	Op protein - Kenne
269	125.5	4.0	635	2	F75477	hypothetical prote	342	120.5	3.8	753	2	JQ0532	internalin, peptid
270	125.5	4.0	764	2	A40077	thyrotropin recept	343	120.5	3.8	821	2	AB1126	disease resistance
271	125.5	4.0	1003	2	T05898	hypothetical prote	344	120.5	3.8	855	2	T17460	probable receptor -
272	125	4.0	350	2	S22456	hydroxyproline-ric	345	120.5	3.8	976	2	B84659	protein kinase hom
273	125	4.0	476	2	A36478	surface glycoprote	346	120.5	3.8	976	2	T05897	receptor protein k
274	125	4.0	783	2	T45899	hypothetical prote	347	120.5	3.8	981	2	T50851	receptor protein k
275	125	4.0	818	2	F96586	hypothetical prote	348	120.5	3.8	987	2	T50850	mucin, tracheobron
276	125	4.0	991	2	T52400	receptor-like prot	349	120.5	3.8	1118	2	A48292	microtubule-associ
277	125	4.0	1504	2	T49896	glycine/proline-ri	350	120.5	3.8	1152	2	A33183	protein FltC7.4 [i
278	125	4.0	2026	1	OYBY	adenylate cyclase	351	120.5	3.8	1722	2	E99753	internalin protein
279	124.5	4.0	298	2	B35272	osteoinductive fac	352	120.5	3.8	1778	2	AF1116	tenascin-X precurs
280	124.5	4.0	756	2	T27642	hypothetical prote	353	120.5	3.8	3566	1	A40701	internalin protein
281	124.5	4.0	849	2	C97303	hypothetical prote	354	120	3.8	361	2	AH1469	probable cell wall
282	124.5	4.0	910	2	G84648	probable disease r	355	120	3.8	376	2	S71558	hypothetical prote
283	124.5	4.0	977	2	C96745	hypothetical prote	356	120	3.8	458	2	T31631	SH3 domains-contai
284	124.5	4.0	1223	2	E88451	protein K10D2.1 [i	357	120	3.8	892	2	T09071	receptor-like prot
285	124.5	4.0	2176	2	T13806	toucan gene protei	358	120	3.8	962	2	T04124	hypothetical prote
286	124	4.0	496	2	D75261	conserved hypothet	359	120	3.8	1126	2	T20801	webi protein homol
287	124	4.0	543	2	S35047	mucin JUL7 - human	360	120	3.8	1224	2	T40765	cell wall glycopro
288	124	4.0	574	2	T43556	Wiskott-Aldrich sy	361	119.5	3.8	267	2	S08314	transcription fact
289	124	4.0	605	2	AGU123	probable antigenic	362	119.5	3.8	479	1	A31753	receptor protein k
290	124	4.0	729	2	F70803	hypothetical prote	363	119.5	3.8	660	2	T45569	large structural p
291	124	4.0	766	2	B85440	receptor kinase-li	364	119.5	3.8	1049	1	XPBEA9	probable receptor
292	124	4.0	978	2	E96787	protein T4Q12.5 [i	365	119.5	3.8	1079	2	C96772	protein F20N2.4 [i
293	124	4.0	1011	2	T45718	receptor-kinase li	366	119.5	3.8	1166	2	F96598	hypothetical prote
294	124	4.0	1472	2	B54774	ATP binding casset	367	119.5	3.8	1400	2	B70963	190K DNA-binding p
295	124	4.0	4135	2	T46629	tenascin-X - bovin	368	119.5	3.8	1596	2	A35927	versican precursor
296	123.5	3.9	380	2	T01281	probable leucine-r	369	119.5	3.8	1643	2	T14274	mucin SAC - human
297	123.5	3.9	492	2	F86263	hypothetical prote	370	119	3.8	164	2	I53641	AWJ1172 protein -
298	123.5	3.9	656	2	AE1479	probable cell surf	371	119	3.8	352	2	S49299	hypothetical prote
299	123.5	3.9	690	2	T41296	hypothetical prote	372	119	3.8	424	2	S27783	hypothetical prote
300	123	3.9	528	2	T15198	wiskott-aldrich sy	373	119	3.8	550	2	C75557	hypothetical prote
301	123	3.9	574	2	T38819	ufo protein - mous	374	119	3.8	651	2	T42644	BHLFI protein - hu
302	123	3.9	888	2	S23065	microtubule-associ	375	119	3.8	660	1	Q0BE3	hypothetical prote
303	123	3.9	1072	2	A37127	pristinamycin I sy	376	119	3.8	808	2	T23129	hypothetical prote
304	123	3.9	2591	2	T30288	hydroxyproline-ric	377	119	3.8	864	2	D84740	hypothetical prote
305	122.5	3.9	303	2	S28264	hypothetical prote	378	119	3.8	1006	2	T42731	atrophin-1 relate
306	122.5	3.9	415	2	T13435	hypothetical prote	379	119	3.8	1045	2	T41119	internalin- relate
307	122.5	3.9	592	2	D70863	hypothetical prote	380	118.5	3.8	222	2	H96711	hypothetical prote
308	122.5	3.9	699	2	T05225	extensin homolog F	381	118.5	3.8	400	1	A39822	leukostallin precu
309	122.5	3.9	809	2	B84634	probable receptor-	382	118.5	3.8	677	2	E70722	hypothetical prote
310	122.5	3.9	845	2	T12537	hypothetical prote	383	118.5	3.8	751	2	AC2098	hypothetical prote
311	122.5	3.9	1016	2	T30553	disease resistance	384	118.5	3.8	869	2	A71400	probable disease r
312	122.5	3.9	2944	2	A54849	collagen alpha 1(V	385	118.5	3.8	883	2	S57653	precavan precursor
313	122	3.9	298	2	JC4130	osteoglycin precu	386	118.5	3.8	988	2	T45717	receptor-kinase li
314	122	3.9	326	2	T24722	hypothetical prote	387	118.5	3.8	1173	2	T25893	hypothetical prote
315	122	3.9	596	2	AE1515	internalin like pr	388	118.5	3.8	1356	2	A45445	janusin precursor,
316	122	3.9	623	2	T19876	hypothetical prote	389	118.5	3.8	1607	2	T02837	long chain fatty a
317	122	3.9	672	2	B84782	probable receptor-	390	118	3.8	294	2	A37232	mucin, tracheal (A
318	122	3.9	715	2	G86239	protein F20B24.6 [	391	118	3.8	599	2	T10798	phosphorin-S - Vo
319	122	3.9	719	2	T47727	hypothetical prote	392	118	3.8	667	2	S74254	homeotic protein s
320	122	3.9	921	2	B86234	hypothetical prote	393	118	3.8	823	2	AD1935	general secretion
321	122	3.9	992	2	T05335	hypothetical prote	394	118	3.8	1134	1	UN0711	protein-tyrosine k

395	118	3.8	2471	2	A49128	cell-fate determin	468	114	3.6	378	2	S00842	leukosialin precu
396	117.5	3.7	473	2	D85041	hypothetical prote	469	114	3.6	413	1	A34888	transcription fact
397	117.5	3.7	624	2	A55576	collagen alpha 2(X	470	114	3.6	555	1	S20100	mullerian inhibiti
398	117.5	3.7	660	2	JW0067	chitinase (EC 3.2.	471	114	3.6	586	2	T29695	hypothetical prote
399	117.5	3.7	996	2	T10725	protein kinase Xa2	472	114	3.6	633	2	S62057	proline-rich prote
400	117.5	3.7	1075	2	T70568	hypothetical prote	473	114	3.6	634	2	T00388	hypothetical prote
401	117.5	3.7	1706	2	I84499	zinc finger protei	474	114	3.6	656	2	E75468	hypothetical prote
402	117	3.7	431	2	T27904	hypothetical prote	475	114	3.6	768	2	A42755	p-selectin precurs
403	117	3.7	655	1	A46688	hepatocyte growth	476	114	3.6	1290	2	T00018	period protein hom
404	117	3.7	670	2	H96707	probable receptor	477	114	3.6	2225	2	T26063	hypothetical prote
405	117	3.7	678	2	JC4245	transcription fact	478	113.5	3.6	317	2	S55316	mucin (clone PGW-2
406	117	3.7	743	2	C84633	probable disease r	479	113.5	3.6	330	2	T46256	brevican - human (
407	117	3.7	801	2	T29018	hypothetical prote	480	113.5	3.6	538	2	T01102	disease resistance
408	117	3.7	1007	2	C84668	probable receptor-	481	113.5	3.6	896	2	B43817	transforming prote
409	117	3.7	1009	2	D75399	probable penicilli	482	113.5	3.6	907	2	A86460	99.9K hypothetical
410	117	3.7	1328	2	T43060	agrin - electric r	483	113.5	3.6	938	1	Q08E24	nuclear antigen EB
411	117	3.7	1450	2	T30273	hypothetical prote	484	113.5	3.6	1286	2	T33476	hypothetical prote
412	117	3.7	1574	2	T13954	MEGF6 protein - ra	485	113.5	3.6	1907	2	S50893	protein-tyrosine-p
413	117	3.7	2082	2	T37056	probable multi-dom	486	113.5	3.6	2911	2	T20566	hypothetical prote
414	117	3.7	2332	2	T34434	hypothetical prote	487	113	3.6	371	2	T49908	hypothetical prote
415	116.5	3.7	279	2	S53363	mucin 5AC (clone J	488	113	3.6	372	2	A48018	mucin 7 precursor,
416	116.5	3.7	439	2	S51939	chitinase (EC 3.2.	489	113	3.6	382	2	E84527	hypothetical prote
417	116.5	3.7	621	2	I39467	low density lipopr	490	113	3.6	419	2	A90888	hypothetical prote
418	116.5	3.7	787	2	T27632	hypothetical prote	491	113	3.6	419	2	H85729	hypothetical prote
419	116.5	3.7	794	2	T27633	hypothetical prote	492	113	3.6	603	2	A75373	probable N-acetyl
420	116.5	3.7	828	2	A88860	protein ZC518.3 [i	493	113	3.6	979	2	A35913	regulatory factor
421	116.5	3.7	1048	2	T31425	C-terminal domain-	494	113	3.6	982	2	A53253	microtubule-associ
422	116.5	3.7	1446	1	A45344	immediate-early pr	495	113	3.6	1002	2	T46033	receptor protein k
423	116.5	3.7	2229	2	T16199	hypothetical prote	496	113	3.6	1025	2	T45647	nuclear antigen EB
424	116	3.7	292	2	S24169	mucin - rat	497	113	3.6	1069	2	S27922	neural plakophilin
425	116	3.7	652	2	S71753	repellent protein	498	113	3.6	1247	2	T42209	cell division prot
426	116	3.7	660	2	AH2348	hypothetical prote	499	113	3.6	1343	2	Af0611	alpha-A-crystallin
427	116	3.7	729	2	F86308	Similar to disease	500	113	3.6	2688	2	T49477	versican precursor
428	116	3.7	771	2	T02565	disease resistance	501	113	3.6	3381	2	T42389	mucin 1 precursor,
429	116	3.7	808	2	B97303	hypothetical prote	502	112.5	3.6	347	2	S10571	unknown protein T1
430	116	3.7	845	2	T07039	Hcr-0 protein - t	503	112.5	3.6	581	2	G96811	hypothetical prote
431	116	3.7	907	2	A24938	hypothetical T2 pr	504	112.5	3.6	731	2	B86369	transcription fact
432	116	3.7	1291	2	T00019	period protein hom	505	112.5	3.6	1075	2	A57377	transcription fact
433	116	3.7	1494	2	T14355	protein-tyrosine-p	506	112.5	3.6	1237	2	AC1583	internalin protein
434	116	3.7	1840	2	T30250	Grl protein - mous	507	112.5	3.6	1680	2	T01367	hypothetical prote
435	116	3.7	2531	2	A46019	notch-1 protein -	508	112.5	3.6	2479	2	F87386	conserved hypotet
436	116	3.7	2555	2	A40043	notch protein homo	509	112.5	3.6	4006	2	T09070	probable tenascin
437	116	3.7	2724	2	A43359	microtubule-associ	510	112	3.6	241	2	S32359	glial growth facto
438	115.5	3.7	322	2	AC53715	apomucin precursor	511	112	3.6	252	2	T01787	thyrotropin recept
439	115.5	3.7	513	2	AC3061	hypothetical prote	512	112	3.6	253	1	JC1319	thyrotropin recept
440	115.5	3.7	513	2	D98225	hypothetical prote	513	112	3.6	285	2	A41826	probable pheromone
441	115.5	3.7	528	2	I47141	gastric mucin (clo	514	112	3.6	383	2	S53716	delta-like homeoti
442	115.5	3.7	696	2	T42659	hypothetical prote	515	112	3.6	413	2	S48756	transcription fact
443	115.5	3.7	805	2	T49385	hypothetical prote	516	112	3.6	704	2	A52107	serine/threonine k
444	115.5	3.7	946	2	S27921	nuclear antigen EB	517	112	3.6	731	2	T04455	hypothetical prote
445	115.5	3.7	1093	2	I38533	AF17 protein - hum	518	112	3.6	742	2	F84643	hypothetical prote
446	115.5	3.7	1268	2	S52781	neurocan - mouse	519	112	3.6	764	1	QRHURH	thyrotropin recept
447	115.5	3.7	1460	1	EDBEIF	immediate-early pr	520	112	3.6	883	2	S49126	brevican precursor
448	115.5	3.7	2214	2	T16305	hypothetical prote	521	112	3.6	960	2	G84652	probable receptor-
449	115.5	3.7	3421	1	WZBBE6	367K tegument prot	522	112	3.6	990	2	T03784	probable receptor
450	115	3.7	404	2	T08549	hypothetical prote	523	112	3.6	1032	2	T34433	hypothetical prote
451	115	3.7	451	2	S74728	hypothetical prote	524	112	3.6	1289	2	AE2217	hypothetical prote
452	115	3.7	461	2	T10741	extensin-like prot	525	111.5	3.6	224	2	D72861	Gene BCRF2 protein
453	115	3.7	479	1	S22542	transcription fact	526	111.5	3.6	383	2	S32975	AcOrf-91 protein -
454	115	3.7	539	2	AH1216	internalin, probab	527	111.5	3.6	478	1	I47154	transcription fact
455	115	3.7	766	2	T01817	hypothetical prote	528	111.5	3.6	645	2	T05251	probable disease r
456	115	3.7	838	2	T08423	Axin homolog Axll	529	111.5	3.6	649	2	T46500	hypothetical prote
457	115	3.7	980	2	T05414	protein kinase hom	530	111.5	3.6	1047	2	A55617	masquerade precurs
458	115	3.7	1133	2	E86308	hypothetical prote	531	111.5	3.6	1253	2	T45787	disease resistance
459	115	3.7	1320	2	A56136	jagged protein pre	532	111.5	3.6	1298	1	EDBE75	immediate-early pr
460	115	3.7	2415	1	A39086	aggreacan precursor	533	111.5	3.6	1353	1	JH0675	restrictin precurs
461	114.5	3.7	328	2	JQ0985	hydroxyproline-ric	534	111.5	3.6	2649	2	T51023	hypothetical prote
462	114.5	3.7	409	2	T17433	pp47 protein - pig	535	111	3.5	274	2	JC8063	heart-restricted l
463	114.5	3.7	505	2	AC1469	internalin like pr	536	111	3.5	478	2	H86459	hypothetical prote
464	114.5	3.7	606	2	T51880	hypothetical prote	537	111	3.5	509	2	T05260	probable disease r
465	114.5	3.7	627	2	T27123	hypothetical prote	538	111	3.5	518	2	S50465	PAC2 protein - yea
466	114.5	3.7	638	2	T05606	protein kinase hom	539	111	3.5	548	2	E70546	hypothetical prote
467	114	3.6	218	2	T01104	disease resistance	540	111	3.5	603	2	S28941	coagulation factor

541	111	3.5	610	2	S35049	mucin JER57 - huma	614	109	3.5	2809	2	T30213	G-cadherin - sea u
542	111	3.5	620	2	T50150	yeast nrd1-like pr	615	108.5	3.5	308	2	JC7125	epidermal growth f
543	111	3.5	699	1	QRHU50	lutropin-choriogon	616	108.5	3.5	389	2	S27200	proline-rich prote
544	111	3.5	853	2	T17461	disease resistance	617	108.5	3.5	402	2	A84581	probable disease r
545	111	3.5	932	2	T21338	hypothetical prote	618	108.5	3.5	418	2	T15142	hypothetical prote
546	111	3.5	984	2	T48216	hypothetical prote	619	108.5	3.5	499	2	A11107	internalin E limpo
547	111	3.5	1721	1	I38902	retinoblastoma bin	620	108.5	3.5	514	2	H70699	probable ppp prote
548	111	3.5	2524	1	A35844	Xotch protein - Af	621	108.5	3.5	548	1	I37577	islet cell antigen
549	110.5	3.5	359	2	C55066	tyrosine decarboxy	622	108.5	3.5	662	2	A45155	mucin FIM-C.1 - Af
550	110.5	3.5	421	2	A60058	neural cell adhesi	623	108.5	3.5	698	2	I39713	celb protein - Agr
551	110.5	3.5	512	2	G86459	Hypothetical 55.6	624	108.5	3.5	710	1	Q8BE22	membrane antigen g
552	110.5	3.5	525	1	A58674	neurotrophin-3 rec	625	108.5	3.5	740	2	B84741	hypothetical prote
553	110.5	3.5	533	2	T07970	aromatic-L-amino-a	626	108.5	3.5	756	2	G8C308	Similar to disease
554	110.5	3.5	565	2	JEO338	Frizzled-2 protein	627	108.5	3.5	764	2	A35956	thyrotropin recept
555	110.5	3.5	684	2	T01267	leucine-rich repea	628	108.5	3.5	783	1	A38637	Ras interactor RIN
556	110.5	3.5	803	1	S35695	neurotrophin-3 rec	629	108.5	3.5	825	1	A40026	neurotrophin-3 rec
557	110.5	3.5	815	2	B56708	extracellular sign	630	108.5	3.5	855	2	C82983	hypothetical prote
558	110.5	3.5	855	2	T07015	Cf-4A protein - to	631	108.5	3.5	1011	2	C84524	probable disease r
559	110.5	3.5	872	2	S33015	hypothetical prote	632	108.5	3.5	1125	2	B41206	microtubule-associ
560	110.5	3.5	992	2	A31666	hypothetical prote	633	108.5	3.5	1176	2	T49482	hypothetical prote
561	110.5	3.5	1207	2	T00378	KIAA0641 protein -	634	108.5	3.5	1184	2	G01763	atrophin-1 - human
562	110.5	3.5	1295	2	A32901	glp1 protein precu	635	108.5	3.5	1344	1	A35175	mucin 1 precursor,
563	110.5	3.5	1344	2	T14316	rig-1 protein - mo	636	108.5	3.5	1357	2	T29265	hypothetical prote
564	110.5	3.5	1346	2	T17412	polyketide synthas	637	108.5	3.5	1487	2	T02850	hypothetical prote
565	110.5	3.5	1736	2	T00391	hypothetical prote	638	108.5	3.5	3707	2	S18252	heparan sulfate pr
566	110.5	3.5	2476	2	T34022	zonadhesin - pig	639	108	3.4	348	2	JQ0431	hypothetical 35.5K
567	110	3.5	275	2	T51437	hypothetical prote	640	108	3.4	409	2	AG0752	flagellar hook-len
568	110	3.5	391	2	T04609	hypothetical prote	641	108	3.4	511	1	VGBE1K	glycoprotein C - h
569	110	3.5	549	2	S32987	hypothetical prote	642	108	3.4	542	2	I39540	chitinase [EC 3.2.
570	110	3.5	591	2	D84889	probable receptor-	643	108	3.4	544	2	T17547	proline-rich prote
571	110	3.5	708	2	D96711	hypothetical prote	644	108	3.4	550	2	T36746	probable serine/th
572	110	3.5	719	2	T02154	protein kinase hom	645	108	3.4	638	1	XXAV	dihydrolipoamide S
573	110	3.5	764	2	I49882	thyrotropin recept	646	108	3.4	741	2	T05250	probable disease r
574	110	3.5	846	2	H70599	hypothetical prote	647	108	3.4	862	2	S43922	versican - pig-tai
575	110	3.5	846	2	T21700	hypothetical prote	648	108	3.4	996	2	JEO237	apolipoprotein E r
576	110	3.5	951	2	A96770	receptor-like prot	649	108	3.4	1017	2	T31354	probable potassium
577	110	3.5	1123	2	D96756	F6F3.12 protein -	650	108	3.4	1217	2	T51140	disease resistance
578	110	3.5	1483	2	E86148	protein-tyrosine-p	651	108	3.4	1217	2	T51141	disease resistance
579	110	3.5	1711	1	A55148	notch protein - fr	652	108	3.4	2783	1	A41948	alpha-fetoprotein
580	110	3.5	2703	1	A24420	eyelid - fruit fly	653	108	3.4	3511	2	A59295	unconventional myo
581	110	3.5	2715	2	T13049	Bassoon protein -	654	108	3.4	4613	2	T17409	polyketide synthas
582	110	3.6	3942	2	T42730	hypothetical prote	655	108	3.4	7576	2	T17428	FK506 polyketide s
583	109.5	3.5	213	2	A86228	hypothetical prote	656	107.5	3.4	363	2	H87702	hypothetical prote
584	109.5	3.5	279	2	T10361	hypothetical prote	657	107.5	3.4	369	2	S20500	hydroxyproline-ric
585	109.5	3.5	318	2	T29479	hypothetical prote	658	107.5	3.4	414	2	C96770	hypothetical prote
586	109.5	3.5	428	2	E71415	probable coll wall	659	107.5	3.4	427	2	S74211	PAS-6/7 protein pr
587	109.5	3.5	473	2	S36553	L2 protein - human	660	107.5	3.4	536	2	H71563	hypothetical prote
588	109.5	3.5	507	2	T44768	antifreeze glycope	661	107.5	3.4	604	2	S25203	srms protein - Str
589	109.5	3.5	538	2	S57459	hook-containing pr	662	107.5	3.4	655	2	G96524	protein TIN15.9 (i
590	109.5	3.5	558	2	JCS5878	plasma hyaluronan-	663	107.5	3.4	832	2	A31246	neurogenic repetit
591	109.5	3.5	583	1	S22544	transcription fact	664	107.5	3.4	880	2	S00670	cellulose synthase
592	109.5	3.5	612	2	I71633	gene trkC protein	665	107.5	3.4	881	2	B98320	receptor kinase-li
593	109.5	3.5	825	2	A55178	neurotrophin recep	666	107.5	3.4	1009	2	T45645	tumor suppressor p
594	109.5	3.5	839	1	I73632	neurotrophin-3 rec	667	107.5	3.4	1099	2	A56155	formin isoform IV
595	109.5	3.5	874	2	E97302	hypothetical prote	668	107.5	3.4	1206	2	S24407	DNA-binding protei
596	109.5	3.5	878	2	T21621	hypothetical prote	669	107.5	3.4	1324	2	S28863	formin - mouse
597	109.5	3.5	954	2	T19765	hypothetical prote	670	107.5	3.4	1468	2	S11515	tegument protein 2
598	109.5	3.5	1299	2	T47182	hypothetical prote	671	107.5	3.4	3534	2	T42567	platelet glycoprot
599	109.5	3.5	1776	1	RRWPYM	genome polyprotein	672	107	3.4	176	1	A46606	extensin-like prot
600	109.5	3.5	2531	2	T31070	notch homolog - se	673	107	3.4	228	2	S53504	fibronectin - chic
601	109.5	3.5	2717	2	A34203	DNA-binding protei	674	107	3.4	273	2	A28512	transmembrane glyc
602	109	3.5	379	2	T05441	proline-rich prote	675	107	3.4	354	2	A48931	transmembrane gly
603	109	3.5	379	2	D85257	extensin-like prot	676	107	3.4	358	1	WMBE38	infected cell prot
604	109	3.5	395	2	I52842	CD43 Lp-3 antigen	677	107	3.4	416	1	SKXLAG	dermal gland prote
605	109	3.5	395	2	A43545	leukosialin CD43 p	678	107	3.4	447	2	A39321	mucin - rat (fragm
606	109	3.5	403	2	S52796	prp12 protein - hu	679	107	3.4	452	2	C41602	transcription fact
607	109	3.5	426	2	JQ1696	pistil extensin-li	680	107	3.4	518	2	F75460	hypothetical prote
608	109	3.5	431	2	T04868	hypothetical prote	681	107	3.4	615	1	KFHU12	coagulation factor
609	109	3.5	437	2	A54595	transcription fact	682	107	3.4	650	2	S59630	dysregolcan alpha
610	109	3.5	598	2	C459756	receptor-like prot	683	107	3.4	840	1	S89204	pheromone response
611	109	3.5	613	2	T42671	hypothetical prote	684	107	3.4	915	2	T12526	hypothetical prote
612	109	3.5	833	2	S19087	gene Delta protein	685	107	3.4	1063	1	GNWVR4	structural polypro
613	109	3.5	1611	2	T38236	hypothetical prote	686	107	3.4	1376	2	G00043	osteonidogen - hum

687	107	3.4	1389	2	I58157	periaxin - rat	760	105	3.3	1133	2	A54164	sterol regulatory
688	107	3.4	2723	2	T03221	probable polyketid	761	105	3.3	1135	2	T30561	scythe protein - A
689	107	3.4	7463	2	T36248	CDA peptide synthe	762	105	3.3	1136	1	S57845	protein-tyrosine k
690	106.5	3.4	3043	2	A32993	transcription fact	763	105	3.3	1456	2	T01397	LTR gag/pol polypr
691	106.5	3.4	353	2	A41558	N-syndecan - rat (	764	105	3.3	1658	2	D75489	hypothetical prote
692	106.5	3.4	505	2	B46629	mucin 6, gastric (	765	105	3.3	1844	2	S01956	hypothetical prote
693	106.5	3.4	509	2	D86911	conserved hypotet	766	105	3.3	2133	2	T30637	hypothetical prote
694	106.5	3.4	509	2	T10013	probable phosphor	767	105	3.3	2409	1	A60979	versican precursor
695	106.5	3.4	517	2	AD1570	interleukin, probab	768	105	3.3	2769	1	UIBO	thyroglobulin prec
696	106.5	3.4	620	2	S06733	hydroxyproline-ric	769	104.5	3.3	329	2	T17033	hypothetical prote
697	106.5	3.4	827	2	AC2963	celb protein [limp	770	104.5	3.3	407	2	C70816	hypothetical prote
698	106.5	3.4	925	2	H95638	protein Tlf9.20 [i	771	104.5	3.3	464	2	T35943	probable hydrolyti
699	106.5	3.4	988	2	C75489	conserved hypotet	772	104.5	3.3	530	2	T32812	hypothetical prote
700	106.5	3.4	1003	2	T13856	ksr protein - frui	773	104.5	3.3	639	2	G02919	transcription fact
701	106.5	3.4	1161	2	S57180	probable membrane	774	104.5	3.3	662	2	T04856	hypothetical prote
702	106.5	3.4	1184	2	S08332	atrophin-1 - human	775	104.5	3.3	700	2	A42395	hypothetical prote
703	106.5	3.4	1305	2	AB0168	probable cell divi	776	104.5	3.3	707	1	A34458	gelatinase B (EC 3
704	106.5	3.4	1442	2	T42607	transcription acti	777	104.5	3.3	707	1	A53796	gelatinase B (EC 3
705	106.5	3.4	1892	2	T18314	hypothetical prote	778	104.5	3.3	744	2	T35192	probable ABC trans
706	106.5	3.4	2090	2	S26058	probable transform	779	104.5	3.3	755	2	T20950	hypothetical prote
707	106.5	3.4	2453	2	S60254	nuclear receptor c	780	104.5	3.3	909	1	QRXLL1	LDL receptor 1 pre
708	106	3.4	135	2	T49996	AtAGP4 - Arabidops	781	104.5	3.3	960	1	S28262	kinesin-related pr
709	106	3.4	167	2	A33532	mucin SMUC-40 - hu	782	104.5	3.3	1117	2	JC4934	delta-crystallin/E
710	106	3.4	216	2	I51920	mucin - rhesus mac	783	104.5	3.3	1194	2	E96624	hypothetical prote
711	106	3.4	287	2	S55765	chitinase (EC 3.2.	784	104.5	3.3	1241	2	T37190	nephrin - human
712	106	3.4	405	2	S78691	flagellar hook-len	785	104.5	3.3	1505	2	JC4851	hypoxia-inducible
713	106	3.4	431	2	S47538	acrosin (EC 3.4.21	786	104.5	3.3	1851	2	T19964	hypothetical prote
714	106	3.4	435	2	D41602	transcription fact	787	104.5	3.3	1898	2	S46216	leukocyte antigen-
715	106	3.4	443	2	A39794	transcription fact	788	104.5	3.3	2117	2	T36180	CDA peptide synthe
716	106	3.4	449	2	B24993	cellulase (EC 3.2.	789	104	3.3	232	2	A60095	larval glue protei
717	106	3.4	567	2	A45977	Rab geranylgeranyl	790	104	3.3	306	2	I49139	lymphotoxin-beta -
718	106	3.4	666	2	B70803	hypothetical prote	791	104	3.3	318	2	B64900	hypothetical prote
719	106	3.4	701	2	D48613	gag polyprotein -	792	104	3.3	326	2	A46676	CD68 homolog macro
720	106	3.4	818	2	T01105	disease resistance	793	104	3.3	332	2	S43988	protein phosphatas
721	106	3.4	822	2	T51049	related to nucleol	794	104	3.3	360	2	S68209	sda22 protein homo
722	106	3.4	850	2	S56015	gastric mucin MUC5	795	104	3.3	365	2	A39481	serum response fac
723	106	3.4	901	2	A49227	sialidase - Actino	796	104	3.3	426	2	D88103	protein W10G11.6 [
724	106	3.4	914	2	T17233	hypothetical prote	797	104	3.3	440	2	I49681	glyceraldehyde-3-p
725	106	3.4	1064	2	A40136	fibropellin fa - s	798	104	3.3	470	2	S36536	L2 protein - human
726	106	3.4	1603	2	A48613	gag/pol polyprotei	799	104	3.3	537	2	A46611	myosin-binding pro
727	106	3.4	1958	2	B40505	hypothetical prote	800	104	3.3	538	2	S65764	chitinase (EC 3.2.
728	106	3.4	2554	1	TVPF7L	kinase-related pro	801	104	3.3	593	2	S49525	glycoprotein G - s
729	106	3.4	3938	2	T42761	Bassoon protein-	802	104	3.3	712	1	I46031	gelatinase B (EC 3
730	105.5	3.4	395	2	T01392	leucine-rich repea	803	104	3.3	895	2	S20582	dyscrophin-asocia
731	105.5	3.4	486	2	A41537	DNA-binding protei	804	104	3.3	927	2	T24031	hypothetical prote
732	105.5	3.4	510	2	A42750	insulinoma-asocia	805	104	3.3	1045	2	T16275	hypothetical prote
733	105.5	3.4	668	2	T05257	probable disease r	806	104	3.3	1547	2	T28657	blackjack protein,
734	105.5	3.4	688	2	T04568	protein kinase hom	807	104	3.3	1575	2	S68448	synaptojanin, 170K
735	105.5	3.4	695	2	S62400	amphiphysin (clone	808	104	3.3	1711	2	T31337	1,4-beta-glucanase
736	105.5	3.4	772	2	T13078	KiA0992 protein -	809	104	3.3	1744	2	A54970	tensin, cardiac mu
737	105.5	3.4	780	2	A48143	HF-1 regulatory el	810	104	3.3	3507	2	T34513	hypothetical prote
738	105.5	3.4	952	2	S32954	hypothetical prote	811	103.5	3.3	206	1	NBHUIB	platelet glycoprot
739	105.5	3.4	1132	2	A35098	MHC class III hist	812	103.5	3.3	264	2	P00478	pistil extensin-li
740	105.5	3.4	1172	2	T00065	hypothetical prote	813	103.5	3.3	281	2	D70845	hypothetical prote
741	105.5	3.4	1621	2	T15264	hypothetical prote	814	103.5	3.3	393	2	P00479	pistil extensin-li
742	105.5	3.4	1712	2	A38261	masking protein pr	815	103.5	3.3	411	1	I55604	platelet glycoprot
743	105.5	3.4	1839	1	RRWPEM	genome polyprotein	816	103.5	3.3	419	2	T49292	hypothetical prote
744	105.5	3.4	2477	2	S14428	fibronectin precu	817	103.5	3.3	444	1	A39794	transcription fact
745	105.5	3.4	3033	1	JQ1303	genome polyprotein	818	103.5	3.3	489	2	F75591	p49 secreted prote
746	105	3.3	349	2	T05857	hypothetical prote	819	103.5	3.3	625	2	A26456	nicotinic acetylch
747	105	3.3	422	2	I37891	interleukin-1l rec	820	103.5	3.3	654	2	T33044	hypothetical prote
748	105	3.3	454	2	E75291	probable cell wall	821	103.5	3.3	889	2	F96637	hypothetical prote
749	105	3.3	460	2	T33110	hypothetical prote	822	103.5	3.3	898	2	T20123	hypothetical prote
750	105	3.3	486	1	A57601	transcription fact	823	103.5	3.3	968	2	T00353	hypothetical prote
751	105	3.3	511	1	VG8EF4	glycoprotein C - h	824	103.5	3.3	975	2	I48974	receptor-protein t
752	105	3.3	566	2	T34842	probable transfera	825	103.5	3.3	980	2	S54986	regulatory protein
753	105	3.3	620	2	T0525	hypothetical prote	826	103.5	3.3	1020	2	A29355	fibronectin - chic
754	105	3.3	658	2	T08153	cysteine proteinas	827	103.5	3.3	1144	2	A54810	TMV resistance pro
755	105	3.3	730	2	JC1456	gelatinase B (EC 3	828	103.5	3.3	1171	2	T35548	hypothetical prote
756	105	3.3	764	2	JC5643	thyroid stimulatn	829	103.5	3.3	1268	2	T31420	C-terminal domain-
757	105	3.3	847	1	A53800	mixed-lineage prot	830	103.5	3.3	1590	2	B86398	protein T7N9.24 [i
758	105	3.3	895	2	I54343	dysoglycan - hum	831	103.5	3.3	1603	2	S23810	collagen alpha 1(X
759	105	3.3	976	2	A36355	protein-tyrosine k	832	103.5	3.3	1638	2	A42091	transcription acti

833	103.5	3.3	1733	1	B45344	probable nuclear a	906	102	3.3	567	2	JC5538	Rab geranylgeranyl
834	103.5	3.3	3739	2	T17410	polyketide synthas	907	102	3.3	585	1	B70747	probable serine/th
835	103	3.3	168	2	S52994	arabinogalactan-li	908	102	3.3	650	2	B87791	protein B0207.1 li
836	103	3.3	191	2	E84740	hypothetical prote	909	102	3.3	670	2	S22293	zinc finger protei
837	103	3.3	227	2	T27905	hypothetical prote	910	102	3.3	715	2	T12534	hypothetical prote
838	103	3.3	263	2	S01360	salivary glue prot	911	102	3.3	722	2	I48324	DELTA-like 1 - mou
839	103	3.3	362	2	A44083	meq protein - Mare	912	102	3.3	728	2	D86278	hypothetical prote
840	103	3.3	367	2	AC1328	internalin protein	913	102	3.3	890	2	E84846	probable receptor-
841	103	3.3	379	2	T16213	APX-1 protein homo	914	102	3.3	896	1	A35782	cytokine receptor
842	103	3.3	394	2	C84905	probable extensin	915	102	3.3	923	2	A35926	progesterone recep
843	103	3.3	515	2	F70904	hypothetical prote	916	102	3.3	963	2	A55926	DNA binding protei
844	103	3.3	535	1	S76953	protein kinase (EC	917	102	3.3	1008	2	T04462	hypothetical prote
845	103	3.3	550	2	G70597	probable proteinas	918	102	3.3	1021	2	H75423	hypothetical prote
846	103	3.3	575	2	JG0181	Xill2 protein - hu	919	102	3.3	1032	2	D83637	serine/threonine p
847	103	3.3	611	2	B86387	unknown protein [i	920	102	3.3	1052	2	B49120	protein-tyrosine k
848	103	3.3	648	2	T35120	hypothetical prote	921	102	3.3	1069	2	D85383	hypothetical prote
849	103	3.3	701	2	F48613	gag polyprotein -	922	102	3.3	1137	2	A85335	T20H2.9 protein -
850	103	3.3	793	2	JC7390	thyroid stimulat	923	102	3.3	1166	2	T13958	synGAP-b1 protein
851	103	3.3	799	1	TVRTTB	nerve growth facto	924	102	3.3	1249	2	T14270	Ras-GTPase activat
852	103	3.3	813	2	T04313	protein kinase Xa2	925	102	3.3	1293	2	T14259	ras-GTPase-activat
853	103	3.3	851	2	S67285	NUD1 protein - yea	926	102	3.3	1692	2	A33988	adenylate cyclase
854	103	3.3	863	2	A55173	cf-9 protein precu	927	102	3.3	1985	2	S19151	hypothetical prote
855	103	3.3	915	2	S36327	clathrin assembly	928	102	3.3	2218	2	B84683	hypothetical prote
856	103	3.3	1040	2	T23092	TSC-22 protein hom	929	102	3.3	2437	2	S42612	transmembrane prot
857	103	3.3	1121	2	A82809	exodeoxyribonuclea	930	102	3.3	2440	2	S39161	transcription coac
858	103	3.3	1199	2	A40670	nuclear envelope p	931	102	3.3	2441	2	S39161	CREB-binding prote
859	103	3.3	1201	2	G86441	unknown protein [i	932	102	3.3	3124	2	A40020	collagen alpha 1(X
860	103	3.3	1275	2	T33369	hypothetical prote	933	102	3.3	5147	1	LJPF7M	cadherin-related t
861	103	3.3	1340	2	A39808	proteoglycan core	934	101.5	3.2	98	2	S53367	mucin SAC (clone M
862	103	3.3	1541	2	T02831	AAA protein L4171.	935	101.5	3.2	173	2	T47176	hypothetical prote
863	103	3.3	1894	2	C54689	protein-tyrosine-p	936	101.5	3.2	244	2	A40428	non-specific cross-
864	103	3.3	2207	1	GNNY5P	genome polyprotein	937	101.5	3.2	372	2	T29359	hypothetical prote
865	103	3.3	2481	2	A43908	fibronectin - Afri	938	101.5	3.2	409	2	T43599	yop targeted effec
866	103	3.3	3133	2	S52093	hemocytin - silkw	939	101.5	3.2	547	2	B56573	nuclear pore compl
867	102.5	3.3	217	2	S01358	salivary glue prot	940	101.5	3.2	654	2	C87587	hypothetical prote
868	102.5	3.3	252	2	T04739	hypothetical prote	941	101.5	3.2	657	2	B84869	probable Sfl6 prot
869	102.5	3.3	316	2	T31880	hypothetical prote	942	101.5	3.2	710	2	T44753	hypothetical prote
870	102.5	3.3	338	2	IS3043	transforming prote	943	101.5	3.2	728	2	IS0719	C-Delta-1 - chicke
871	102.5	3.3	352	2	S17313	transcription fact	944	101.5	3.2	733	2	A87168	conserved hypother
872	102.5	3.3	371	2	F70555	hypothetical prote	945	101.5	3.2	833	2	A22089	hypothetical prote
873	102.5	3.3	379	2	S31719	proline-rich prote	946	101.5	3.2	869	2	A55384	transcription fact
874	102.5	3.3	383	2	B86272	protein Fl6A14.12	947	101.5	3.2	921	2	S40495	collagen alpha 1(I
875	102.5	3.3	385	2	S53718	homeotic protein d	948	101.5	3.2	947	2	G85420	probable receptor-
876	102.5	3.3	385	2	A54785	preadipocyte facto	949	101.5	3.2	977	2	IS2657	seizure-related pr
877	102.5	3.3	421	2	T30709	core protein homol	950	101.5	3.2	984	1	A34076	protein-tyrosine k
878	102.5	3.3	507	1	A32385	erythropoietin rec	951	101.5	3.2	1034	2	JC5569	serine proteinase
879	102.5	3.3	627	2	D75393	serine proteinase,	952	101.5	3.2	1039	2	A85096	hypothetical prote
880	102.5	3.3	674	2	T05264	probable serine/th	953	101.5	3.2	1429	2	S06434	homeotic protein 1
881	102.5	3.3	706	2	E30411	synapsin Ia - bovi	954	101.5	3.2	1668	2	T13748	sex comb protein -
882	102.5	3.3	730	1	IS2580	gelatinase B (EC 3	955	101.5	3.2	1733	2	S27939	tensin - chicken
883	102.5	3.3	760	1	S07896	disease resistance	956	101.5	3.2	4543	1	A53102	alpha-2-macroglobu
884	102.5	3.3	904	2	T46170	hypothetical prote	957	101	3.2	240	2	B24264	proline-rich prote
885	102.5	3.3	907	2	E96636	hypothetical prote	958	101	3.2	249	2	S72619	hypothetical prote
886	102.5	3.3	942	1	JQ1674	protein kinase TMK	959	101	3.2	294	2	T34537	hypothetical prote
887	102.5	3.3	964	2	JC5545	integrin beta-4 pr	960	101	3.2	360	2	S25561	transcription fact
888	102.5	3.3	1013	2	T46422	hypothetical prote	961	101	3.2	373	2	A44478	probable cell grow
889	102.5	3.3	1115	1	IJWSNL	neural cell adhesi	962	101	3.2	401	2	A48423	engrailed homeodom
890	102.5	3.3	1233	2	T15316	hypothetical prote	963	101	3.2	482	2	A44997	merozoite surface
891	102.5	3.3	1350	2	G36793	hypothetical prote	964	101	3.2	492	2	B86911	probable penicilli
892	102.5	3.3	1367	1	S48478	glucan 1,4-alpha-g	965	101	3.2	570	2	B87619	sensor histidine k
893	102.5	3.3	1678	2	T35547	hypothetical prote	966	101	3.2	612	2	A28798	myosin-light-chain
894	102.5	3.3	1779	2	T31085	xylanase - Caldice	967	101	3.2	613	2	A40497	dihydrolipoamide S
895	102.5	3.3	1813	2	T30564	resistance protein	968	101	3.2	615	1	XXHU	dihydrolipoamide S
896	102.5	3.3	1863	2	S46217	protein-tyrosine-p	969	101	3.2	628	2	JQ0110	hypothetical 69K p
897	102.5	3.3	1875	2	A36429	integrin beta-4 ch	970	101	3.2	671	2	D84648	probable disease r
898	102.5	3.3	2207	2	S09553	genome polyprotein	971	101	3.2	688	2	T18263	S-layer protein -
899	102	3.3	301	2	JQ1663	hybrid proline-ric	972	101	3.2	700	2	D70951	probable UvrD - My
900	102	3.3	307	2	S36779	ribosome-binding p	973	101	3.2	739	2	IS6187	transcription fact
901	102	3.3	317	2	A28996	proline-rich prote	974	101	3.2	796	2	T21460	hypothetical prote
902	102	3.3	353	2	B38963	bcsA 5'-region pro	975	101	3.2	846	1	QBEC3	HQRFL protein - hu
903	102	3.3	413	2	T49545	hypothetical prote	976	101	3.2	1043	2	A56037	DNA-binding protei
904	102	3.3	532	2	S74453	hypothetical prote	977	101	3.2	1127	2	T32404	hypothetical prote
905	102	3.3	554	1	FQHUMP	macrophage colony-	978	101	3.2	1257	2	S28764	neurocan precursor

979	101	3.2	1367	2	T33819	hypothetical prote	1052	99.5	3.2	352	2	S05500	Ig alpha-1 chain C
980	101	3.2	1513	2	A54895	mucin 2, intestina	1053	99.5	3.2	353	1	AIHU	Ig alpha-1 chain C
981	101	3.2	1792	2	A57075	tensin - chicken (	1054	99.5	3.2	353	2	S36438	EPF1 protein - hyd
982	101	3.2	2946	2	T15840	hypothetical prote	1055	99.5	3.2	375	1	TDHUM4	monocyte surface g
983	101	3.2	3176	2	CGHU3A	collagen alpha 3(I	1056	99.5	3.2	383	1	VGBERG	glycoprotein precu
984	100.5	3.2	1378	2	D96715	protein F4N2.10 li	1057	99.5	3.2	387	2	B49175	Mock A protein -
985	100.5	3.2	2136	2	T33408	hypothetical prote	1058	99.5	3.2	392	2	B48423	homeotic protein e
986	100.5	3.2	262	2	E88400	protein H34124.2 l	1059	99.5	3.2	393	1	VGBED2	glycoprotein D - h
987	100.5	3.2	269	2	T28957	hypothetical prote	1060	99.5	3.2	420	2	T46910	hypothetical prote
988	100.5	3.2	274	2	T46041	hypothetical prote	1061	99.5	3.2	451	2	JC4199	heat-shock protein
989	100.5	3.2	283	2	E88597	protein Y47D3B.6 l	1062	99.5	3.2	476	1	C70986	probable serine/th
990	100.5	3.2	314	2	T48514	hypothetical prote	1063	99.5	3.2	491	2	F70699	probable pbpA prot
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat	1064	99.5	3.2	530	2	S52215	hypothetical prote
992	100.5	3.2	401	2	S65138	glycoprotein antiq	1065	99.5	3.2	539	2	T28770	hypothetical prote
993	100.5	3.2	440	2	JC7807	Wiskott-Aldrich sy	1066	99.5	3.2	647	2	T43952	hypothetical prote
994	100.5	3.2	504	2	AG2373	hypothetical prote	1067	99.5	3.2	665	2	S62328	hypothetical prote
995	100.5	3.2	512	2	S56745	mucin (clone pGM31	1068	99.5	3.2	702	2	A86383	kinesin-like DNA b
996	100.5	3.2	504	2	E59437	F02569.2 protein l	1069	99.5	3.2	802	2	T24293	76.4K protein kina
997	100.5	3.2	597	2	JQ0107	hypothetical 66K p	1070	99.5	3.2	851	2	AD1427	internalin, probab
998	100.5	3.2	677	2	T39713	zinc finger protei	1071	99.5	3.2	853	1	IJBONC	neural cell adhesi
999	100.5	3.2	798	2	T34248	hypothetical prote	1072	99.5	3.2	886	2	T35469	probable ATP /GTP-
1000	100.5	3.2	906	2	A43817	transforming prote	1073	99.5	3.2	903	2	T19209	probable protein k
1001	100.5	3.2	975	2	S33121	homeotic protein C	1074	99.5	3.2	949	2	T24294	hypothetical prote
1002	100.5	3.2	1024	2	T27631	hypothetical prote	1075	99.5	3.2	958	2	B82994	glycine cleavage s
1003	100.5	3.2	1030	2	H88859	protein ZC518.2 li	1076	99.5	3.2	961	1	TSHUP4	thrombospondin 4 p
1004	100.5	3.2	1106	1	TVHUGL	transforming prote	1077	99.5	3.2	1013	2	T33470	hypothetical prote
1005	100.5	3.2	1131	2	F96662	hypothetical prote	1078	99.5	3.2	1016	2	T41720	hypothetical prote
1006	100.5	3.2	1138	1	S24066	protein-tyrosine k	1079	99.5	3.2	1056	2	A53767	mucin MUC5B, trach
1007	100.5	3.2	1220	2	T48928	disease resistance	1080	99.5	3.2	1122	2	T47424	hypothetical prote
1008	100.5	3.2	1273	2	S58782	SEC31 protein - ye	1081	99.5	3.2	1220	2	T06403	resistance complex
1009	100.5	3.2	1323	2	T30253	spalt protein - mo	1082	99.5	3.2	1390	2	T31353	polyprotein - Arab
1010	100.5	3.2	2327	2	T42630	aggreca - bovine	1083	99.5	3.2	1473	2	T31422	C-terminal domain-
1011	100.5	3.2	2862	2	T14266	xin protein - chic	1084	99.5	3.2	1742	2	T17120	cellulase (EC 3.2.
1012	100.5	3.2	3562	2	A47171	chondroitin sulfat	1085	99.5	3.2	3869	2	A48205	All-1 protein +GrE
1013	100.5	3.2	4548	1	S00657	apoptein(a) (EC	1086	99	3.2	154	2	PQ0476	pistil extensin-li
1014	100	3.2	230	2	A56210	neu differentiatio	1087	99	3.2	214	2	T09854	proline-rich cell
1015	100	3.2	311	2	B86211	hypothetical prote	1088	99	3.2	307	1	GSFF3	salivary glue prot
1016	100	3.2	334	2	G02409	protein kinase C-b	1089	99	3.2	329	2	B41344	lutropin-choriogon
1017	100	3.2	366	2	S61796	T-cell-specific tr	1090	99	3.2	329	2	D41344	lutropin-choriogon
1018	100	3.2	367	2	A33950	YopM protein - Yer	1091	99	3.2	331	2	C41344	lutropin-choriogon
1019	100	3.2	474	2	S15921	protein TPX-VT3 -	1092	99	3.2	358	2	T01296	leucine-rich repea
1020	100	3.2	476	2	C39481	serum response fac	1093	99	3.2	415	1	A34170	acrosin (EC 3.4.21
1021	100	3.2	510	2	H84824	En/Spm-like transp	1094	99	3.2	428	2	S45361	LRB47 protein - fr
1022	100	3.2	535	2	T17212	hypothetical prote	1095	99	3.2	447	2	T34992	probable lipoprote
1023	100	3.2	549	2	C87719	protein R119.6 lim	1096	99	3.2	466	2	T06416	cysteine proteinas
1024	100	3.2	556	2	T070940	probable PPE prote	1097	99	3.2	511	2	AC0941	probable ABC trans
1025	100	3.2	562	2	S75308	DNA ligase (EC 6.5	1098	99	3.2	543	2	S25128	61K protein - Auto
1026	100	3.2	596	2	G75457	tetratricopeptide	1099	99	3.2	564	2	I53106	gene gli protein -
1027	100	3.2	628	2	S44138	polyadenylate-bind	1100	99	3.2	569	2	F75381	probable two-compo
1028	100	3.2	673	2	AF1143	internalin protein	1101	99	3.2	616	2	C75588	conserved hypothet
1029	100	3.2	698	2	T51915	hypothetical prote	1102	99	3.2	638	2	T51383	receptor protein k
1030	100	3.2	698	2	T17261	hypothetical prote	1103	99	3.2	641	2	C84726	probable receptor-
1031	100	3.2	699	2	T09069	probable cAMP-resp	1104	99	3.2	686	2	F96542	probable protein k
1032	100	3.2	713	2	T44447	neuregulin-3 limpo	1105	99	3.2	696	2	A41344	lutropin-choriogon
1033	100	3.2	725	2	T01268	leucine-rich repea	1106	99	3.2	701	2	S61239	hypothetical prote
1034	100	3.2	756	2	C87432	hypothetical prote	1107	99	3.2	770	1	S30293	transcription fact
1035	100	3.2	776	2	A46583	neuroendocrine-spe	1108	99	3.2	814	2	JC7389	thyroid stimulat
1036	100	3.2	881	2	T01269	serine/threonine-s	1109	99	3.2	860	2	C86203	hypothetical prote
1037	100	3.2	1109	2	C84545	probable disease r	1110	99	3.2	940	2	H86420	probable receptor-
1038	100	3.2	1161	2	T45294	hypothetical prote	1111	99	3.2	963	2	T19140	hypothetical prote
1039	100	3.2	1182	2	I48378	hairless protein -	1112	99	3.2	1000	2	C82630	serine proteinase
1040	100	3.2	1240	2	T08404	resistance complex	1113	99	3.2	1097	2	T49187	hypothetical prote
1041	100	3.2	1420	2	T37781	probable cytoskele	1114	99	3.2	1147	2	T42627	ADP-ribosylation f
1042	100	3.2	1687	2	T30176	EGF repeat transme	1115	99	3.2	1217	2	T52348	disease resistance
1043	100	3.2	1791	2	T02345	hypothetical prote	1116	99	3.2	1317	2	T03748	apoptosis associat
1044	100	3.2	1802	2	T00020	bacterial blight-r	1117	99	3.2	1405	2	T04426	hypothetical prote
1045	100	3.2	1897	1	TDHULK	leukocyte antigen-	1118	99	3.2	1532	2	A61262	collagen alpha 1(X
1046	100	3.2	2459	2	AF2136	peptide synthetase	1119	99	3.2	1538	2	E70874	probable ppsB prot
1047	99.5	3.2	108	2	S08315	cell wall protein	1120	99	3.2	1694	2	S50065	sialoadhesin - mou
1048	99.5	3.2	177	2	T07642	PEARL1 protein h	1121	99	3.2	1799	1	S44920	ZK688.5 protein -
1049	99.5	3.2	230	2	A44074	probable EGF-like	1122	99	3.2	2029	1	TDFFLK	protein-tyrosine-p
1050	99.5	3.2	280	2	I48713	Phox2 homeodomain	1123	99	3.2	2088	2	E71436	hypothetical prote
1051	99.5	3.2	293	2	C75421	hypothetical prote	1124	99	3.2	6420	2	T30283	polyketide synthas

1125	98.5	3.1	230	2	T22763	hypothetical prote	1198	97.5	3.1	362	2	S22395	fetuin precursor -
1126	98.5	3.1	254	2	D88560	protein F58A4.1 [i	1199	97.5	3.1	429	2	JC4965	elk1 protein - mou
1127	98.5	3.1	342	2	I77461	luteinizing hormon	1200	97.5	3.1	460	2	T23087	hypothetical prote
1128	98.5	3.1	349	2	T15422	hypothetical prote	1201	97.5	3.1	464	2	S22697	extensin - Volvox
1129	98.5	3.1	379	2	S50125	larval glue protei	1202	97.5	3.1	497	2	F83634	hypothetical prote
1130	98.5	3.1	385	2	T18180	proline-rich prote	1203	97.5	3.1	511	2	T43282	alpi1 protein - fi
1131	98.5	3.1	393	2	S62335	171-7 protein - fr	1204	97.5	3.1	521	2	S54266	glycoprotein gc -
1132	98.5	3.1	434	1	A35005	u-plasminogen acti	1205	97.5	3.1	531	2	B55066	tyrosine decarboxy
1133	98.5	3.1	464	2	D72653	hypothetical prote	1206	97.5	3.1	563	2	A75594	ferredoxin-nitrite
1134	98.5	3.1	486	2	B39481	serum response fac	1207	97.5	3.1	574	1	A48501	probable protein-1
1135	98.5	3.1	514	2	A44100	cell adhesion mole	1208	97.5	3.1	587	2	T41653	probable transcrip
1136	98.5	3.1	633	2	T47346	receptor protein k	1209	97.5	3.1	614	2	T33149	hypothetical prote
1137	98.5	3.1	700	2	I77463	luteinizing hormon	1210	97.5	3.1	626	2	B70754	probable serine/th
1138	98.5	3.1	700	2	A49744	lutropin-choriogon	1211	97.5	3.1	627	1	JC6534	protein kinase 1 (
1139	98.5	3.1	707	2	A46302	PTB-associated spl	1212	97.5	3.1	627	2	AB0535	hypothetical prote
1140	98.5	3.1	770	2	T22808	hypothetical prote	1213	97.5	3.1	631	1	A36749	transcription fact
1141	98.5	3.1	803	2	F59433	RhOGAP protein [im	1214	97.5	3.1	662	2	D40228	neurexin II-beta p
1142	98.5	3.1	837	2	A42112	mucin-like peptide	1215	97.5	3.1	676	1	EDBE23	immediate-early pr
1143	98.5	3.1	862	2	B88594	protein Y48A6B.11	1216	97.5	3.1	710	2	D96728	hypothetical prote
1144	98.5	3.1	885	2	B86257	NBS/LRR disease re	1217	97.5	3.1	754	2	AC2807	OmpA family protei
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -	1218	97.5	3.1	754	2	B97586	hypothetical prote
1146	98.5	3.1	947	2	T26314	hypothetical prote	1219	97.5	3.1	814	2	G02390	disintegrin-like m
1147	98.5	3.1	1087	2	T31100	probable potassium	1220	97.5	3.1	817	2	S51342	verprolin - yeast
1148	98.5	3.1	1272	2	T30248	fragile X mental r	1221	97.5	3.1	830	2	T17672	chitinase-like pro
1149	98.5	3.1	1281	2	T00346	hypothetical prote	1222	97.5	3.1	893	2	H96651	protein T3P18.19 [
1150	98.5	3.1	1309	2	T00078	probable RNA-direc	1223	97.5	3.1	909	1	A54809	disease resistance
1151	98.5	3.1	1396	2	A44453	translation initia	1224	97.5	3.1	921	2	AE0332	conserved hypothet
1152	98.5	3.1	1774	2	B56101	collagen alpha 1(X	1225	97.5	3.1	929	2	T52517	hypothetical prote
1153	98.5	3.1	2180	2	T29764	hypothetical prote	1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1154	98.5	3.1	2339	2	A42566	omega-conotoxin-se	1227	97.5	3.1	1006	2	G86292	hypothetical prote
1155	98	3.1	182	2	T07641	PEARL1 protein h	1228	97.5	3.1	1258	2	JC5765	inositol polyphosp
1156	98	3.1	291	2	AF0123	probable antigenic	1229	97.5	3.1	1392	2	T51947	probable transcrip
1157	98	3.1	296	2	A56943	sensory/motor neur	1230	97.5	3.1	1715	2	C40228	neurexin II-alpha
1158	98	3.1	303	2	S40973	hypothetical prote	1231	97.5	3.1	1748	1	J01555	genome polyprotein
1159	98	3.1	352	2	S09266	Ig alpha chain C r	1232	97	3.1	191	2	F84522	probable proline-r
1160	98	3.1	416	1	A42879	advanced glycosyla	1233	97	3.1	238	2	T23867	hypothetical prote
1161	98	3.1	442	2	S50062	cell wall glycopro	1234	97	3.1	238	2	T26419	hypothetical prote
1162	98	3.1	499	2	A12449	hypothetical prote	1235	97	3.1	330	2	T05717	probable extensin
1163	98	3.1	514	2	A56201	transcription fact	1236	97	3.1	355	2	B26883	neural cell adhesi
1164	98	3.1	534	2	S21961	proline-rich prote	1237	97	3.1	357	2	A39364	GDF-1 embryonic gr
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.	1238	97	3.1	379	2	AE3003	conserved hypothet
1166	98	3.1	538	2	I68093	PRR2 delta - human	1239	97	3.1	395	2	A86166	protein F2IB7.6 [i
1167	98	3.1	538	2	A70836	hypothetical prote	1240	97	3.1	397	2	T00914	leucine-rich repea
1168	98	3.1	553	1	A42499	mullerian inhibiti	1241	97	3.1	400	1	A38172	spasmolysin precu
1169	98	3.1	560	1	WFHUM	mullerian inhibiti	1242	97	3.1	421	1	S11674	acrosin (EC 3.4.21
1170	98	3.1	605	2	S48940	hypothetical prote	1243	97	3.1	428	1	TVHUEK	transforming prote
1171	98	3.1	614	2	S27962	modulator recognit	1244	97	3.1	452	2	D98280	hypothetical 28.0K
1172	98	3.1	631	2	C89243	protein F28C1.3 [i	1245	97	3.1	459	2	T35317	probable serine/th
1173	98	3.1	631	2	T21471	hypothetical prote	1246	97	3.1	483	2	T02226	NBS-LRR type resis
1174	98	3.1	715	2	S76492	lipoprotein nlpD -	1247	97	3.1	500	2	D97302	hypothetical prote
1175	98	3.1	728	2	H59435	phosphoinositide-3	1248	97	3.1	530	2	G70904	hypothetical prote
1176	98	3.1	750	2	T42614	probable envelope	1249	97	3.1	601	2	D89711	protein F40E10.4 [
1177	98	3.1	788	1	Q3BEE3	HLHFI protein - hu	1250	97	3.1	601	2	T22025	hypothetical prote
1178	98	3.1	856	2	T43631	serine/threonine k	1251	97	3.1	632	2	T02627	hypothetical prote
1179	98	3.1	889	2	C86257	resistance to pseu	1252	97	3.1	701	1	FCV1LR	gag polyprotein -
1180	98	3.1	896	2	S36326	clathrin assembly	1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1181	98	3.1	1006	2	JC5526	kinase-defective E	1254	97	3.1	966	2	D96662	hypothetical prote
1182	98	3.1	1216	2	T34101	hypothetical prote	1255	97	3.1	967	2	G96637	hypothetical prote
1183	98	3.1	1372	2	T25933	hypothetical prote	1256	97	3.1	1123	2	A39962	kinase-related tra
1184	98	3.1	1522	2	H88380	protein T22F7.3 [i	1257	97	3.1	1214	2	T47438	disease resistance
1185	98	3.1	1873	2	A55645	calcium channel, v	1258	97	3.1	1265	1	A37967	neural cell adhesi
1186	98	3.1	2115	2	S38480	nonstructural prot	1259	97	3.1	1690	2	T35694	ATP dependent DNA
1187	98	3.1	2190	2	T13828	CREB-binding prote	1260	97	3.1	1734	2	A54602	microtubule-associ
1188	98	3.1	3623	2	T08618	intrinsic factor-B	1261	97	3.1	2055	2	T00093	hypothetical prote
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch	1262	97	3.1	2205	1	GNNY2W	genome polyprotein
1190	98	3.1	3871	2	T22812	hypothetical prote	1263	97	3.1	3034	2	T14119	seven-pass transme
1191	98	3.1	5069	2	T17464	rifamycin polyketi	1264	96.5	3.1	346	2	S19129	proline-rich prote
1192	97.5	3.1	215	2	S55925	probable arabinoga	1265	96.5	3.1	350	2	E75341	peptidyl-prolyl ci
1193	97.5	3.1	266	1	A35037	insulin-like growt	1266	96.5	3.1	419	2	G70602	hypothetical prote
1194	97.5	3.1	268	2	S71830	transcription coac	1267	96.5	3.1	430	2	I48755	mSAPla - mouse
1195	97.5	3.1	277	2	A46241	interferon respons	1268	96.5	3.1	444	2	B36389	transcription fact
1196	97.5	3.1	306	2	T09067	extensin-like prot	1269	96.5	3.1	485	1	S22543	transcription fact
1197	97.5	3.1	338	1	TVMSFB	transforming prote	1270	96.5	3.1	487	2	F70765	hypothetical prote

1271	96.5	3.1	514	2	A31643	cell adhesion 80k	1344	95.5	3.0	1159	2	138465	probable potassium
1272	96.5	3.1	528	2	B75310	conserved hypotet	1345	95.5	3.0	1255	2	T31065	diaphanous protein
1273	96.5	3.1	574	2	B35149	ipah protein - Shi	1346	95.5	3.0	1256	2	T03096	CDO protein - rat
1274	96.5	3.1	598	2	T42070	protein serine/thr	1347	95.5	3.0	1331	2	T49813	related to gastric
1275	96.5	3.1	635	2	F70874	probable membrane	1348	95.5	3.0	1630	2	T00390	KIAA0614 protein -
1276	96.5	3.1	637	2	A75342	hypothetical prote	1349	95.5	3.0	2761	2	T21064	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote	1350	95	3.0	175	2	138408	neu differentiation
1278	96.5	3.1	654	2	T45017	chemotaxis histidi	1351	95	3.0	227	2	C29149	proline-rich prote
1279	96.5	3.1	669	2	T08827	hypothetical prote	1352	95	3.0	227	2	G70555	hypothetical prote
1280	96.5	3.1	796	2	E96654	hypothetical prote	1353	95	3.0	239	2	S25618	hypothetical prote
1281	96.5	3.1	825	1	EDBEXD	immediate-early pr	1354	95	3.0	241	2	D43273	heregulin precuro
1282	96.5	3.1	1021	2	A86421	Receptor-like seri	1355	95	3.0	273	2	C70551	hypothetical prote
1283	96.5	3.1	1209	2	T00373	hypothetical prote	1356	95	3.0	326	2	A52332	ABA-responsive pro
1284	96.5	3.1	1241	2	T18311	hypothetical prote	1357	95	3.0	338	2	T06336	proline-rich prote
1285	96.5	3.1	1557	2	T02859	probable serine/th	1358	95	3.0	385	1	I39498	GTP cyclohydrolase
1286	96.5	3.1	2282	2	T42717	DNA-binding protei	1359	95	3.0	413	2	T52617	hypothetical prote
1287	96.5	3.1	2352	2	T30201	Notch homolog prot	1360	95	3.0	477	2	S53362	mucin 5AC (clone J
1288	96.5	3.1	26926	1	I38344	titin, cardiac mus	1361	95	3.0	494	1	A29079	lymphocyte surface
1289	96	3.1	214	2	T10737	extensin-like cell	1362	95	3.0	502	2	A55197	Wiskott-Aldrich sy
1290	96	3.1	240	2	A24264	proline-rich prote	1363	95	3.0	636	2	I61718	neu differentiation
1291	96	3.1	287	2	T75494	cell division prote	1364	95	3.0	653	2	E84682	hypothetical prote
1292	96	3.1	346	2	JA0159	cysteine proteinas	1365	95	3.0	662	2	I61722	neu differentiation
1293	96	3.1	445	2	T05887	hypothetical prote	1366	95	3.0	667	2	T17221	hypothetical prote
1294	96	3.1	451	2	D88395	protein P53A3.6 li	1367	95	3.0	673	2	T48012	hypothetical prote
1295	96	3.1	483	2	S12741	transcription fact	1368	95	3.0	705	2	A35621	spore germination
1296	96	3.1	537	1	FOWGVV	gag polyprotein -	1369	95	3.0	712	2	G02512	interleukin-1 rece
1297	96	3.1	580	2	T43481	probable mucin DKF	1370	95	3.0	760	2	T16726	hypothetical prote
1298	96	3.1	594	2	S33561	ref(2)P protein -	1371	95	3.0	776	2	C96554	unknown protein li
1299	96	3.1	598	2	T48822	hypothetical prote	1372	95	3.0	799	2	T48889	serine/threonine p
1300	96	3.1	635	1	WMBE66	capsid protein - h	1373	95	3.0	846	2	S52418	GTP-binding regula
1301	96	3.1	858	1	IJRTNC	neural cell adhesi	1374	95	3.0	891	2	G84693	probable proline-r
1302	96	3.1	883	2	A96662	hypothetical prote	1375	95	3.0	901	2	A44825	phosphoprotein, sy
1303	96	3.1	907	2	AD2951	cell division prote	1376	95	3.0	903	2	S60257	meltrin alpha - mo
1304	96	3.1	910	2	H98331	cell division prote	1377	95	3.0	943	2	T34847	probable transcript
1305	96	3.1	969	2	A75634	McxB-related prote	1378	95	3.0	1024	2	S18251	collagen alpha 1(X
1306	96	3.1	1216	2	T26104	hypothetical prote	1379	95	3.0	1209	2	T13153	brahma associated
1307	96	3.1	1231	2	S30185	insulin receptor s	1380	95	3.0	1324	2	T14070	peptide synthetase
1308	96	3.1	1344	2	E59431	phosphoinositide-b	1381	95	3.0	1474	2	B85188	retrotransposon li
1309	96	3.1	1615	2	B49502	protein-tyrosine-p	1382	95	3.0	1616	2	G70668	polyketide synthas
1310	96	3.1	1737	2	T00209	MEGF8 protein - hu	1383	95	3.0	1731	2	AB3045	ice nucleation pro
1311	96	3.1	1767	2	I19502	protein-tyrosine-p	1384	95	3.0	1731	2	B98241	hypothetical prote
1312	96	3.1	1844	1	RRWPTM	genome polyprotein	1385	95	3.0	1770	2	T18551	saframycin Mxi syn
1313	96	3.1	2529	2	A56923	transcription fact	1386	95	3.0	1806	1	CGHUIE	collagen alpha 1(X
1314	96	3.1	5376	2	T42215	zonadhesin - mouse	1387	95	3.0	2090	2	T30075	hypothetical prote
1315	95.5	3.0	188	2	D29149	proline-rich prote	1388	95	3.0	2148	2	A56011	transcription fact
1316	95.5	3.0	284	2	F95320	conserved hypotet	1389	95	3.0	2274	2	T30258	adenomatous polyo
1317	95.5	3.0	366	1	TDMSM4	monocyte surface g	1390	95	3.0	3084	1	MMWSA	laminin alpha-1 ch
1318	95.5	3.0	382	2	S75823	threonine synthase	1391	94.5	3.0	211	2	T01381	high sulfur zein p
1319	95.5	3.0	384	2	S51796	vasodilator-stimul	1392	94.5	3.0	255	2	B75309	hypothetical prote
1320	95.5	3.0	435	2	T46443	hypothetical prote	1393	94.5	3.0	255	2	S31096	proline-rich prote
1321	95.5	3.0	451	2	S71754	cellular hepatitis	1394	94.5	3.0	270	2	E87649	hypothetical prote
1322	95.5	3.0	479	2	D70676	probable PE protei	1395	94.5	3.0	277	2	I38857	microtubule-associ
1323	95.5	3.0	486	2	AB2975	succinate semialde	1396	94.5	3.0	298	2	H87533	peptidase, M23/M37
1324	95.5	3.0	486	2	A98308	atcK protein (U594	1397	94.5	3.0	301	2	D87684	transcription regu
1325	95.5	3.0	501	2	S75563	hypothetical prote	1398	94.5	3.0	358	2	A61188	probable transcript
1326	95.5	3.0	507	1	A46713	erythropoietin rec	1399	94.5	3.0	376	2	H82988	hypothetical prote
1327	95.5	3.0	553	2	T53118	hypothetical prote	1400	94.5	3.0	393	2	E82283	conserved hypotet
1328	95.5	3.0	570	2	A48836	fibropallin C prec	1401	94.5	3.0	464	2	A83557	probable amidase P
1329	95.5	3.0	571	2	T43456	hypothetical prote	1402	94.5	3.0	569	2	T19128	hypothetical prote
1330	95.5	3.0	573	2	B70726	probable secD - My	1403	94.5	3.0	630	2	A39344	tumor-associated m
1331	95.5	3.0	624	2	T49366	myocyte-specific e	1404	94.5	3.0	665	2	E75461	probable cell wall
1332	95.5	3.0	630	2	T31798	hypothetical prote	1405	94.5	3.0	708	2	JC4364	gelatinase B (EC 3
1333	95.5	3.0	650	2	S44806	F10E9.6 protein -	1406	94.5	3.0	719	2	T33170	hypothetical prote
1334	95.5	3.0	685	2	S65691	E75 B steroid rece	1407	94.5	3.0	860	2	I48839	tenascin-X - mouse
1335	95.5	3.0	710	1	S70965	serine/threonine-s	1408	94.5	3.0	921	2	S42617	collagen alpha 1(I
1336	95.5	3.0	722	2	T22359	hypothetical prote	1409	94.5	3.0	985	2	T06049	hypothetical prote
1337	95.5	3.0	749	2	E87599	hypothetical prote	1410	94.5	3.0	1006	2	T00050	hypothetical prote
1338	95.5	3.0	790	1	TVHUTT	nerve growth facto	1411	94.5	3.0	1092	1	JN0635	neural cell adhesi
1339	95.5	3.0	880	2	D89756	protein T23E7.2b l	1412	94.5	3.0	1092	1	T13850	gene u-shaped prot
1340	95.5	3.0	943	2	E84429	probable receptor-	1413	94.5	3.0	1487	1	EDBEE1	immediate-early pr
1341	95.5	3.0	987	2	A54092	protein-tyrosine k	1414	94.5	3.0	1690	1	CGHUIB	collagen alpha 4(I
1342	95.5	3.0	1027	2	I38759	zinc finger/leucin	1415	94.5	3.0	2062	2	G96602	probable receptor
1343	95.5	3.0	1054	2	A30239	hydroxymethylgluta	1416	94.5	3.0	2302	2	T14328	protein-tyrosine-p

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1417 94.5 3.0 2386 1 FNHU
1418 2484 2 T26216
1419 94.5 3.0 2607 2 T26215
1420 94 3.0 157 2 T02034
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1422 94 3.0 277 2 E72564
1423 94 3.0 293 2 T22919
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1487 93 3.0 209 2 T02262
1488 93 3.0 221 2 T07079
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hypothetical prote
hypothetical prote
early light-induce
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cytokinin-induced
probable cell surf
hypothetical prote
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probable cell wall
early growth respo
transcription fact
merozoite surface
nucleoporin p62 -
hypothetical prote
hypothetical prote
neu differentiation
whn protein - rat
pectate lyase (EC
serine/threonine-s
hypothetical prote
probable transmemb
major nitrogen reg
probable ABC trans
interleukin-3 rece
fasciclin II precu
scavenger receptor
transcription fact
hypothetical prote
probable membrane
disease resistance
probable regulator
hypothetical prote
TCOF1 protein - mo
mannan endo-1,4-be
racGAP protein - s
gene expanded prot
glutamate synthase
hypothetical prote
hypothetical prote
collagen-related p
hypothetical prote
probable mmp83 pro
hypothetical prote
probable cell wall
cyst wall protein
transcription fact
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tumor necrosis fac
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probable serine/th
poliovirus recepto
serine/threonine p
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receptor-like prot
hypothetical prote
subtilisin-like pr
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protein F12M16.30
LDL receptor 2 pre
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WD-repeat protein
protein H05O09.1 [
hypothetical prote
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high-methionine d-
leucine-rich repea
mucin like protein

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## ALIGNMENTS

## RESULT 1

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JC5239
insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C>Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JC5239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-1:
A:Reference number: JC5239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: JC5239
A:Molecule type: mRNA
A:Residues: 1-605 <DEL>
A:Cross-references: UNIPARC:UPI000000D50E
C:Comment: This factor is structurally related to proinsulin and have insuline-like met-

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Query Match 10.3%; Score 322; DB 2; Length 605;

Best Local Similarity 36.2%; Pred. No. 2e-11; Mismatches 100; Conservative 39; Mismatches 97; Indels 40; Gaps 11;

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QY 7 LLLPLLL--LAIG-----PGVQG-----CPGCGCQSQPQ-----TVFCTARQGT 45
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Db 8 LALALLLSWALGPRSLGEGAEPTGGEAGPACATACSYDDDEVNLSVFCSSNLTFR 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 46 VPRDVPPTVGLYVFENGITMLDASSFAGLPGLQLDLDSQNIASLRPLRL------- 98
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 LPDGIPTGCTQALWLDNNLSSIPPAFRNLSSLAFLNLQGGQLGSLE-PPALLGLENLCH 126
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 99 LDLSHNSLLALEPGLDITANVEALPLAGIG---LQQLDEGLFSRLNHLDLVDSDNQLER 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 LHLERNQLRSRSLAVGTG--AYTPALALLGLSNRLSRLEDGLFEGGLNLDLNGWNSLAV 184
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QY 156 VP-PVIRGLRGLTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPR 214
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## RESULT 2

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A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N:Alternate names: Acid-labile Subunit (ALS)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A41915
R:Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A:Title: Structure and functional expression of the acid-labile subunit of the insulin-1:
A:Reference number: A41915; MUID:92357025; PMID:1379671
A:Accession: A41915
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-605 <LEO>

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A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:gl84807; PIDN:  
A;Experimental source: liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)  
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F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
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F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>  
F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>  
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QY 46 VPRDVPDVTGLYVFNGLTMDASSFAGLPGLQLLDLSQNIASIRLPRILL----- 98  
Db 68 LPDGVPGCTQALMDGNLSSVPPFAFQNLSSLGLFNLQGGQLGSLF-PQALLGLENLCH 126  
  
QY 99 LDLSHNSLLALEPGLDITANVEALRLAGLGL--LQQLDEGLFSRLNLHDLVDVSNQLER 155  
Db 127 LHLENQRLSLALGTF--AHTPALASLGLSNRLSERLEDGLFEGLSGLWDLNGLWNSLAV 184  
  
QY 156 VP-PVIRGLRGLTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLPFR 214  
Db 185 LPDAAFRGLSLRELVLGN--RLAYLPALFSGLAELRELDLSRNALRAIKANVFQLPR 243  
  
QY 215 LRLLLAAANPNFCVPLSFWG-----PWRESHVTLA 246  
Db 244 LQKYLDRNLTAANAAPGAFGLKALRWLDLSHRVA 279  
  
RESULT 3  
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platelet glycoprotein Ib alpha chain precursor - human  
N;Alternate names: membrane glycoprotein Ib alpha chain  
N;Contains: glycoocalicin  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004  
C;Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102  
R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987  
A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p  
A;Reference number: A94174; MUID:87289655; PMID:3303030  
A;Accession: A94174  
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R;Whick, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J.  
Thromb. Haemost. 61, 448-453, 1989  
A;Title: Isolation and characterization of human blood platelet mRNA and construction of  
d cloning of a GPIb coding cDNA insert.  
A;Reference number: A60435; MUID:90020160; PMID:2799758  
A;Accession: A60435  
A;Molecule type: mRNA  
A;Residues: 207-467 <WIC>  
A;Cross-references: UNIPARC:UPI0000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987  
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet men  
A;Reference number: A94173; MUID:87289654; PMID:3497398  
A;Accession: A94173  
A;Molecule type: protein  
A;Residues: 17-315 <TIT>  
A;Cross-references: UNIPARC:UPI0000174312  
R;Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.  
Eur. J. Biochem. 199, 389-393, 1991  
A;Title: Identification of the disulphide bonds in human platelet glycoocalicin.  
A;Reference number: S16945; MUID:91301149; PMID:2070794  
A;Accession: S16945  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 224-227;262-270;277-282 <HES>  
A;Cross-references: UNIPARC:UPI0000174313; UNIPARC:UPI0000174314; UNIPARC:UPI0000174315  
J;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.  
J. Biol. Chem. 267, 10055-10061, 1992  
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t  
ations.  
A;Reference number: I55355; MUID:92250564; PMID:1577776  
A;Accession: I55355  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
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A;Note: variant D  
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates  
C;Comment: Platelet activation apparently involves disruption of the macromolecular com  
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with ur  
C;Comment: Glycoocalicin, which is approximately coextensive with the extracellular part  
C;Genetics:  
A;Gene: GDB:GP1BA; GPIB  
A;Cross-references: GDB:118806; OMIM:231200  
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C;Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)  
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r  
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repe  
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F:94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
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F:502-540/Domain: transmembrane #status predicted <TRM>  
F:541-626/Domain: intracellular #status predicted <INT>  
F:37,175/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:308/Binding site: carbohydrate (Thr) (covalent) #status experimental  
  
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Best Local Similarity 24.0%; Pred. No. 4.4e-09;  
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QY 9 LPLLLLLALGPGVQCPSGCQCSQPT---VFCTARQGTTPRDPVPPDTVGLYVFN--- 62  
Db 1 MPLLLLLLLLLPLPPLPPICEVSKVASHLEVNCENLTALPPDLPKDTTILHLSNLLY 60  
  
QY 63 -----GITWLDASSF-----AGLPGQLLDLSQNIASL-----RLPRLLL 98  
Db 61 TFSLATLMPYTRLTQALNDRCELTKQLQVDGTLFVLGTLDLSHNQLQSLPLLQOTLPALT 120  
  
QY 99 LDLSHNSLLALEPGLT-DTANVEALRLAGLQQLDEGLFSRLNLHDLVDVSNQLERVP 157  
Db 121 LDVSFNRLTSLPLGALRGLGLSELGLLYLKGNELKTLPPGLTPTPKLEKLSLANNLTLP 180  
  
QY 158 P-VIRGLRGLTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSG--LPFR 214  
Db 181 AGLNGLENLDTLLQLQEN-----SLYTIKPGFFGSHLLPFF 215



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Db	16 PELWLLWAAAWRLGATACALCTCT-GTVDCHGTGLQAIKFNTPRNTRELNGNIT 74
QY	66 MLDASSFAGLPLQLLDLSONQIASLRPLRLLLDLSHNSLLALEPGIL-DTANVEALRL 124
Db	75 RIHKNDFAGLKQRLVQLMENOIG-----AVERGAPDDMKELERLRL 116
QY	125 AGLGLQQLDEGLFSRLNLHDLVDSDNQLRVP-PVIRGLRGLTRLRAGNTRIAQLRPE 183
Db	117 NRNLQVLPELLFQNNQALSRDLSENLSQAVPKAFKATDLKNLQDKN-QISCIEEG 175
QY	184 DIAGLAALQELDVSNLSQALPGDLSGLFPRLRLAAARNPNCVCPISWFGPWVRESHV 243
Db	176 AFRALRGLEVLNNNNITIPVSSFNMHPKLRTRFLSHNLFCDCHLAWLSQWLQ-RP 234
QY	244 TLASPEETRCHFPKPNAGRLLELDYADGCPATTTTATVPTTRPVVREPTALSSSLAPT 303
Db	235 TIGL--FTCCSGPASLRGUNAENVOKSEFSCSGQGEAAQVPA-----CTLSSGSCPA 284
QY	304 WLSPTAPATEAPSPSTAPPTVGPVPQO-----DCPSTCLNGTCHLG----- 348
Db	285 MCSCSNGIIVDCRGKGLTAIPANLPETMTETRLLENGIKSIIP-----GAFSPVR 333
QY	349 -----TRHHLACLPCEGFTGLYCESQMGQSTRSPPTVTPRPRSLTGLIEPVS--PT 399
Db	334 KLRRIDLSNQIAETAPDAFOGL-----RSLNSLVLYGNKITDLP 374
QY	400 SURVGLQRYLQSGSVQLRSRLTRYNLSPD--KRLVTLRLPA-----SLAEYTVQL 450
Db	375 GVFGGLY-----TIQLLLLNANKINCRPDADFQDLQNLSSLYDNKIQSLAKGTFTSL 428
QY	451 RPNATYVVCWMP 462
Db	429 RAIQTLHLAQN 440
RESULT 7	
A:Accession: A53531	
N:Alternate names: oncofetal antigen 574	
C:Species: Homo sapiens (man)	
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004	
R:Myers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.	
J. Biol. Chem. 269, 9319-9324, 1994	
A:Title: Isolation of a cDNA encoding 574 oncofetal trophoblast glycoprotein. An antigen	
A:Reference number: A53531; MUID:94179356; PMID:8132670	
A:Accession: A53531	
A:Status: preliminary	
A:Molecule type: mRNA	
A:Residues: 1-420 <WEY>	
A:Cross-references: UNIPROT:Q13641; UNIPARC:UPI000004CAD5; EMBL:229083; NID:G435654; PID	
F:1-31/Domain: signal sequence #status predicted <SIG>	
F:32-420/Product: oncofetal trophoblast glycoprotein 574 #status predicted <MAT>	
Query Match 8.4%; Score 264.5; DB 2; Length 420;	
Best Local Similarity 28.1%; Pred. No. 2.9e-08;	
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;	
QY	2 CSRVP-----LLPLLLLLALG-----PGVQCPS 26
Db	5 CSRGAAGDGRLLARLALVLGVSSSSPTSSASSFSSAPFLASAVSAQPLPDQCPA 64
QY	27 GCQCSQ-PQTVECTARQGTVPDPVPPDTVGLVYVENGITMLDASSFAGLP---GLQLLD 82
Db	65 LCECEAAATVKVNRNTEVETDLPAYVYRNILFLGNQLAVLPAGAFARPPPLAEALN 124
QY	83 LSONQIASLR-----LPRLLLDLSHNSLLALEPGILDANVEALRLAGLQQLDEGL 136

Db	125 LSGSRLDVRAGAPEHLPSLRQLDLSHNPLADLSPPAFSGSNASV-----SAPSP 175
QY	137 FSRLNLHDLVDSDNQLR-----VPPVI--RGLRGLTRLRAGNTRIAQLRPEDLAGL 188
Db	176 VELILN-HIVPPEDERQNRSEFGMVVAALLAGRALQGLRRLLEASN-HFLYLPDRVLAQL 233
QY	189 AALQELDVSNLSQALP-----GDLSGLPPLRLRLAA 220
Db	234 PSRLHDLSDNSLSVLTIVSPFNLTHLSLHLEDNALKVLHNGTTLAEQGL-PHIRVF-L 291
QY	221 ARNPNCVCPISWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGC---PA 276
Db	292 DNNPWCDOCHMADVMYTLKETEV-VQKDRLTCAYPEKMRNVRVLELASADLDCDPIPPP 350
QY	277 TTTTATV 283
Db	351 SLQTSYV 357
RESULT 8	
MEGF5 protein - rat	
N:Alternate names: slit protein homolog	
C:Species: Rattus norvegicus (Norway rat)	
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004	
C:Accession: T13953	
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.	
Genomics 51, 27-34, 1998	
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs	
A:Reference number: Z14126; MUID:98360089; PMID:9693030	
A:Accession: T13953	
A:Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1523 <NAK>	
A:Cross-references: UNIPROT:O88280; UNIPARC:UPI00000E5F7A; EMBL:AB011531; NID:G3449291;	
C:Genetics:	
A:Gene: MEGF5	
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein	
Query Match 8.3%; Score 261; DB 2; Length 1523;	
Best Local Similarity 26.3%; Pred. No. 2e-07;	
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;	
QY	24 CPSCQCSQPTVCTARQGTVPDPVPPDTVGLVYVENGITMLDASSFAGLPGLQLLDL 83
Db	725 CPEQCTCYE-TVVRCNSRGLHTLPKGMKPDVTELYLEGNHLTAV----- 767
QY	84 SONOIASLRPLRLLDLSHNSLLALEPGILDANVEALRLAGLQQLDEGLFSRLNL 143
Db	768 -PKELSTFR--QLTLIDLSNNS-----ISMLTHTFTSNMSHL 801
QY	144 HDLDVSDNQLRVP-PVIRGLRGLTRLRAGNTRIAQLRPEDLAGLALQELDVSNLSQ 202
Db	802 STLILSYNLRACIPVHAFENGLRSRLVTLHGN-----DISSVPEGSFNDLTSL-- 850
QY	203 ALPGDLSGLFRLRLAAARNPNCVCPISWFGPWVRESHVTLASPETRCHFPKPNAGR 262
Db	851 -----HLALGINPLHCDCLSLRWSEWIKAGY---KEPFIARCSSPESMADR 893
QY	263 LLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWTLSPTAPATEAPSPPTAP 322
Db	894 LLLTPTTHRFQCKG-----PVDINIVAKNACLSS--PCKNNGTCQSDPVQVQRCTCP 944
QY	323 PTVGFPVPOPODC--PPSTCL-----NGGCTHLGTRHH--LACLCPGEGFTGLYCE 367
Db	945 YSY----KGKDTVPINTCVQNPQCHGCTCHLSHSDRGFGSCCPLGFEQORCE 994
RESULT 9	
B36665	
slit protein 2 precursor - fruit fly (Drosophila melanogaster)	
C:Species: Drosophila melanogaster	
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002	

C;Accession: B36665  
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.  
Genes Dev. 4, 2169-2187, 1990  
A;Title: slit: an extracellular protein necessary for development of midline glia and cell  
A;Reference number: A36665; MUID:91099665; PMID:2176636  
A;Accession: B36665  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1469 <ROT>  
A;Cross-references: UNIPARC:UPI0000177454; GB:X53959  
C;Genetics:  
A;Gene: FlyBase:slit  
A;Cross-references: FlyBase:FBgn0003425  
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein <PAH1>  
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>  
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>  
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>  
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>  
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>  
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>  
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>  
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>  
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>  
F;1028-1061/Domain: EGF homology <EGF>  
F;1068-1099/Domain: EGF homology <EGF2>  
F;1115-1148/Domain: EGF homology <EGF1>  
Query Match 8.1%; Score 255.5; DB 2; Length 1469;  
Best Local Similarity 21.4%; Pred. No. 3.9e-07;  
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;  
QY 24 CFSGCCSQPQVFCTARQGTTPRDPV-----PDTVGLY 58  
DB 519 CPAMCHC-EGTTVDCGTGRLEKIPRDIPLHTTELLNDNELGRISDGLFGRPLHLVKLE 577  
QY 59 VPENGITMLDASSFAGLPGQLLDLSONOIAS-----LRLPRLLLLDLSHNSLLALEPG 112  
DB 578 LKRNQUTGIEPNAFEGASHIQELQGENKIKESINNOFGLGLHQLKTLNLYDNOISCVMPG 637  
QY 113 ILDTAN-----VEALRLAGLGLQQLDEGLFSRLRLNHLDDV--- 148  
DB 638 SPEHLNLSLNLASPNFNCNLAWFAECVRKSLNGGACGAPSKVRDVQIKDLPHS 697  
QY 149 -----SDNQLERP-----PV----- 159  
DB 698 EFKCSSENSEGLGDGCPSPCTCTGTVVACSRNQLKEIPRGIPAEISLYESNEIEQI 757  
QY 160 ----TRELGLRRLAGNTRIAQLRPEDLAGLAALQELDVS-----NL 199  
DB 758 HYERIKHLSLRLDLS-NNQITILSNYTFANLTKLSTLIISYNKLCQLQRLHALSGLNNL 816  
QY 200 SLQALPGDLSGLFPR-----LRLAAARNPFCVCPLSNFGFPWVRESHYVTLASPBE 251  
DB 817 RVVSLHGNISMLPEGSFEDLSKSLTHIALGNSPLYCDGLKWFSDWKLDYV---EPGTA 873  
QY 252 RCHFPKNAGRLLLELDYADFQCPATTTTATVTPRPVREPTALSSSLAPTWLSFTAPA 311  
DB 874 RCAEPEQMKDKLILSTPSSSFVCRGVRNDILAKGNACFEQPCQNOACV-----ALPQ 927

QY 312 TEAPSPPTAPPTVGPVPOP-----QDCPSTCLNGTCHLGRHHLACLCPG 360  
DB 928 REVQC-----LCQPGVGHKCEFMIDACYGNPCNNATCTVLEGRFSCQCAPG 976  
QY 361 FTGLYCESQM 370  
DB 977 YTGARCETNI 986

## RESULT 10

A36665  
slit protein 1 precursor - fruit fly (*Drosophila melanogaster*)  
C;Species: *Drosophila melanogaster*  
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text\_change 02-Aug-2002  
C;Accession: A36665; A31640; S13523  
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.  
Genes Dev. 4, 2169-2187, 1990  
A;Title: slit: an extracellular protein necessary for development of midline glia and cell  
A;Reference number: A36665; MUID:91099665; PMID:2176636  
A;Accession: A36665  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1480 <ROT>  
A;Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:98614; PIDN:CAA37910.1; PID:G  
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.  
Cell 55, 1047-1059, 1988  
A;Title: slit: An EGF-homologous locus of *D. melanogaster* involved in the development of  
A;Reference number: A31640; MUID:89077533; PMID:3144436  
A;Accession: A31640  
A;Molecule type: DNA  
A;Residues: 881-1182, 'G', 1185-1404, 'GT', 'G', 1463-1464, 'YHA', 'RO2'  
A;Cross-references: UNIPARC:UPI000016BD7A; GB:M23543; NID:9340939; PID:G514357  
C;Genetics:  
A;Gene: FlyBase:slit  
A;Cross-references: FlyBase:FBgn0003425  
A;Introns: 1351/3  
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein  
C;Keywords: alternative splicing; growth factor  
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>  
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>  
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>  
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>  
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>  
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>  
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>  
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>  
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>  
F;1028-1061/Domain: proteoglycan carboxyl-terminal homology <PCS4>  
F;1068-1099/Domain: EGF homology <EGF>  
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1480;  
Best Local Similarity 21.4%; Pred. No. 4e-07;  
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;



QY 199 LSLQALPG-----DLSGLFPLRLLAARPNFNCVCLSWFGPWVRES 241  
DB 235 NSLAWPEGLWASLQPNWMDRGDFDISG-----NFWICDQNLSDLYRWLQAQ 282  
QY 242 HVTLASPEETRCHFPKNGRLL 265  
DB 283 KDKMFSQNDTRCAGPAVKGOTLL 306

RESULT 13  
A60164  
Platelet membrane glycoprotein V precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 12-Jan-1993 #sequence revision 24-Feb-1994 #text change 09-Jul-2004  
C:Accession: A48030; A60164; A35483; B35483; C35483; A60432; A47507; S34329  
R:Lanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T.  
J. Biol. Chem. 268, 20801-20807, 1993  
A:Title: Cloning and characterization of the gene encoding the human platelet glycoprotein V  
A:Reference number: A48030; MUID:94012616; PMID:8407908  
A:Accession: A48030  
A:Molecule type: DNA  
A:Residues: 1-560 <LA2>  
A:Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:g312501; PID:RShimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama, Blood 75, 2349-2356, 1990  
A:Title: Rapid purification and characterization of human platelet glycoprotein V: the a  
A:Reference number: A60164; MUID:90275263; PMID:2350580  
A:Accession: A60164  
A:Molecule type: protein  
A:Residues: 365-384, 'X', 386-390, 'X', 392-395, 'X', 397, 188-208, 'I', 210, 27-50, 'X', 52-53, 174-  
'XX', 108, 'T', 61-72, 'TK', 75-77, 'V', 56-57, 'G', 479-487, 'X', 489-498, 'X', 500, 'X', 502-503, 'X',  
A:Cross-references: UNIPARC:UPI000017C2F6; UNIPARC:UPI000017C2F7; UNIPARC:UPI000017C2F8;  
2FD; UNIPARC:UPI000017C2F9; UNIPARC:UPI000017C2FE; UNIPARC:UPI000017C2FF; UNIPARC:UPI000017C300; UNIPARC:UPI000  
R:Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.  
Biochem. Biophys. Res. Commun. 170, 153-161, 1990  
A:Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a  
A:Reference number: A35483; MUID:90321220; PMID:2372284  
A:Accession: A35483  
A:Molecule type: protein  
A:Residues: 145-166, 'I', 168-169, 'X', 171-172 <ROT>  
A:Cross-references: UNIPARC:UPI000017C303  
A:Note: this proteolytic fragment was designated peptide M392  
A:Accession: B35483  
A:Molecule type: protein  
A:Residues: 121-129, 'W', 131-135, 466-468, 'X', 470 <RO2>  
A:Cross-references: UNIPARC:UPI000017C304; UNIPARC:UPI000017C305  
A:Note: this material was designated peptide M393 but may contain two peptides  
A:Accession: C35483  
A:Molecule type: protein  
A:Residues: 252-266, 'H', 268-272, 'X', 274-279, 'I', 281-284, 'I', 286 <RO3>  
A:Cross-references: UNIPARC:UPI000017C306  
A:Note: this proteolytic fragment was designated peptide M401  
R:Zafar, R.S.; Walz, D.A.  
Thromb. Res. 53, 31-44, 1989  
A:Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl  
A:Reference number: A60432; MUID:89162331; PMID:2922700  
A:Accession: A60432  
A:Molecule type: protein  
A:Residues: 477-478, 'FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498 <ZAF>  
A:Cross-references: UNIPARC:UPI000017C307  
R:Hickey, M.J.; Hagen, F.S.; Yaghi, M.; Roth, G.J.  
Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993  
A:Title: Human platelet glycoprotein V: characterization of the polypeptide and the rela  
A:Reference number: A47507; MUID:93391348; PMID:7690959  
A:Accession: A47507  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-560 <RES>  
A:Cross-references: UNIPARC:UPI000004B117; GB:I11238; NID:g388759; PIDN:AAA03069.1; PID:  
C:Comment: This platelet membrane protein is a substrate for thrombin.  
C:Comment: The amino end of the intact protein is blocked.  
C:Comment: This protein is absent in Bernard-Soulier syndrome.  
C:Genetics:

A:Gene: GDB:GPS  
A:Cross-references: GDB:230236; OMIM:173511  
A:Map position: 5pter-sqter  
C:Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot

Query Match 7.7%; Score 240; DB 2; Length 560;  
Best Local Similarity 27.2%; Pred. NO. 1e-06;  
Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;

QY 57 LYVFENGITMLDASSFAGLPGQLQLDLSONQI-----ASL--RLPRLLLDLHNSILALE 110  
DB 127 LFLDHNAURGIDQNMFKLVNLQELALNQNQLDFLPASLFTNLENKLLDLGNNLTHLP 186  
QY 111 PGILDT-ANVEALRIAGLQQLDDEGL-----FSRLRNLDH 145  
DB 187 KGLLGAQAKLERLLHLSNRVLSLGSLLNSLGAULTLOFHRNHRSIAPGAFDRLPNLS 246  
QY 146 LDVS-----DNQLRVPPVIRG----- 162  
DB 247 LTLSRNHLAFLPSALFLHSHNLTLLTFENPLAELPGVLFGEMGGLQELWLNRTQLTLP 306  
QY 163 ---LRGLTELRAGNT---RTAQLRPEDLAGLAALQELDV----- 196  
DB 307 AAAPFNLSRLRYLGVTLSPRLSALPQGAFOGLGELQVLALHNSNGLTALPDGLLRGLGKLR 366  
QY 197 -----SNLS-----LQALPGDLSGLFPLRLLAARPNFNCV 228  
DB 367 QVSLRRNRLRALPRALFRNLSLSVSQLDHNQLETLPGDVGALPRLTEVLLGHNSWRCD 426  
QY 229 CPLSWFGPWVRESHVTLASPEE-TRCHFPKNGRLLLELDYADFGCPATTTTATVPTTR 287  
DB 427 CGLGFLGLWLRQ-HLGLVGESEPPRCAGPGAGHGLPLWALPGDAECFG-----PRGP 478  
QY 288 PWTREPTLSSSLAPTWSLPTAPATEAPSPSTAPPTVGP 327  
DB 479 P--PRPAADSS-----EAPVHPALAPNSSEP 503

RESULT 14  
JC7763  
Neuronal leucine-rich repeat protein-3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C:Accession: JC7763  
R:Fukamachi, K.; Matsuo, Y.; Kitano, C.; Kuchino, Y.; Tsuda, H.  
Biochem. Biophys. Res. Commun. 287, 257-263, 2001  
A:Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene  
A:Reference number: JC7763; PMID:11549284  
A:Contents: Fibrosarcoma cells  
A:Accession: JC7763  
A:Molecule type: mRNA  
A:Residues: 1-707 <FUK>  
A:Cross-references: UNIPROT:Q9BSY6; UNIPARC:UPI000004F0F2; GB:AF291437  
C:Comment: This protein, a new member of the neuronal leucine-rich repeat  
in protein-protein interaction and functions as a cell adhesion molecule or soluble liga  
C:Genetics:  
A:Gene: nlrr-3  
C:Keywords: cell adhesion

Query Match 7.6%; Score 237; DB 2; Length 707;  
Best Local Similarity 20.7%; Pred. NO. 2e-06;  
Matches 127; Conservative 80; Mismatches 222; Indels 186; Gaps 22;

QY 6 PLLPLLLLLLALGPGVQG-----CPSCQCS-----QPQVFTCARQGTTPV 47  
DB 5 PLQIHVLGLAITALVQAGDKKVCPCQICTCIRPFWFTPRSIYMEASTVDCNDLGLNFP 64  
QY 48 RDVDPDTVGLVFNGLTMDASSFAGLP-GLQLLDLSONQIASL----- 91  
DB 65 ARLPADYQILLQTNNTARIHSHT--DFPNVLTGLDLSQNNLSSVTNINQKMSQLSVY 122  
QY 92 -----RLPRLLLDLDS-----HNSLLALSPGIL----- 114

Db 123 LEENKLTPEKCLYGLSNQLQELVYVNHNLSSAISPGAFVGLHNLRLHLNSNRLQWINSK 182  
QY 115 ---DTANVEALRL-----AGLGLOQLDEGLFSRLNLHOLD 147  
Db 183 WFEALPNLEILMGDNPILRLKDMNFQPLKLSLVIAGINLTVPPDDALVGLNLEGIS 242  
QY 148 VSDNOLERV-----PVIIRGLRG----- 165  
Db 243 FYDNRINKVPQVALQKAVNLKFDLKNKPNIRRGDFSNMHLKELGINNPELVISIDS 302  
QY 166 -----LTRLRAGNTRIAQLRPEDLAGLAQLDVSNLQAL-PGDLISGLFPRLR 216  
Db 303 LAVDNLPDLRKTEATNPNRLSYIHPNAPFLPKLSLMLNSALSALYHGTIESL-PNLK 361  
QY 217 LLAARPNPNCVPLSWFGFWREHVTLASPEETRCHPPKKNAGRLLELDYADFGCPA 276  
Db 362 EISHSNPTRCDVIRWIN--NKNINIREMPEDSLFCVDPPEFQGNVRQVHFRDM---- 415  
QY 277 TTTTATVPTTRPVREPTALSSSL---APTMLSPTAPATEAPSPSTAPPTVGPVPQPD 333  
Db 416 -----MEICLPLI-APESFPSILDVEADSVYSLHCRATAEPQ-----PEIYWIIPSGKR 463  
QY 334 CPPSTCLNGGTCHL-GTRHHLACLCEPGETGLY---CESQMGGTRPSPTVTPRPFR-- 387  
Db 464 LLPNTLREKFVYHSEGTLDIRGITPKEG--GLYTCTATNLVGLADLSIMIKVGGFVPQDN 521  
QY 388 ---SLTIGIEPVSPTSLRVGLQRYLOGSVQLRSRLTYRNLSGPKRLVTLRLPASLAY 445  
Db 522 NGLSNIKIRDIRANSVLVS---WKANSKILKSVKVFVKTEDSQAQASARIPSDVKVY 578  
QY 446 TVTOLRPNATYSVCV 460  
Db 579 NLTHLKPSTYKICI 593

## RESULT 15

T42626  
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)  
N:Alternate names: neurogenic extracellular slit protein  
C:Species: Mus musculus (house mouse)  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T42626  
R:Holmes, G.P.; Negus, K.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.  
Mech. Dev. 79, 57-72, 1998  
A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in  
A:Reference number: Z22177; MUID:99279238; PMID:10349621  
A:Accession: T42626  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1025 <HOL>  
A:Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI0000E8104; EMBL:AF074960; NID:g4151258;  
C:Genetics:  
A:Gene: Slit2  
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 7.4%; Score 231; DB 2; Length 1025;  
Best Local Similarity 24.0%; Pred. No. 6.9e-06;  
Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;  
QY 24 CPSCQCSQPQVFCFARQTTVPRDVPDVTGLYVFENGITMLDASSFAGLPGLQLDL 83  
Db 223 CPSECTCLD-TVRCGSKGLKVLPGIPKDVTELYLDGNOFTLV-PKLSNYKHLTLIDL 280  
QY 84 SQNQIASL-----RLPRLLLDLGHNSLLALEPGILDITANVEALRLAGLGQQLDEGLF 137  
Db 281 SNNRISLNSNOXFSNNQTLLTLISYNLRICPPRTFD-----GLKSL----- 323  
QY 138 SPLRNHLDVDSDNQLRVPPVIRGLRGLRRLAGNTRIAQLRPEDLAGLAQLDVS 197  
Db 324 -RLSLHGNDIS-----VVP----- 337  
QY 198 NLSLQALPGDLISGLFRLRLAAARNPNCVPLSWFGFWREHVTLASPEETRCHPPP 257

Db 338 ----EGAFNDLSA-----LSHLAIGANPLYCDNQMLSDWKSEY---KEPGIARCAGPG 386  
QY 258 KNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP 317  
Db 387 EMADKLLLTTPSKKFTCO-----GPMDDITIAKCNPCLSN 421  
QY 318 PSTAPPTVGPVP-----QPQDCP-----PSTCLNGGTCHL--GTRHHLACL 356  
Db 422 PKNDGTNNDFVDFYRCTCPYGFKGQDCDVIHACISNPCKHGGTCHLKEGENAGFWCT 481  
QY 357 CPEFGTGLYCE 367  
Db 482 CADGFEENCE 492

Search completed: February 7, 2006, 16:18:13  
Job time : 58 secs

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: February 7, 2006, 16:12:51 ; Search time 251 Seconds  
 (without alignments)  
 1680.900 Million cell updates/sec

Title: US-10-677-669-69  
 Perfect score: 3135  
 Sequence: 1 MCSRVELLPLLLALLALPG.....PLMGPPGGLQSPHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Liefting first 1500 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3135	100.0	598	2	Q6UXL5_HUMAN
2	3083.5	98.4	673	2	Q6UXL4_HUMAN
3	3078.5	98.2	673	2	Q6ENK4_HUMAN
4	2697.5	86.0	601	2	Q96CX1_HUMAN
5	2491	79.5	673	2	Q8BJJ0_MOUSE
6	2490	79.4	673	2	Q8RZG5_MOUSE
7	2484	79.2	673	2	Q9CZT5_MOUSE
8	1213.5	38.7	661	2	Q6DF55_XENTR
9	927.5	29.6	643	2	Q503G2_BRARE
10	914.5	29.2	962	2	Q4S068_TETNG
11	368.5	11.8	513	2	Q50LG9_HUMAN
12	359.5	11.5	635	1	LRFN4_HUMAN
13	351	11.2	636	1	LRFN4_MOUSE
14	341	10.9	660	2	Q8BLU0_MOUSE
15	339	10.8	521	2	Q8BHAL_MOUSE
16	338	10.8	655	2	Q4SGV9_TETNG
17	333	10.6	858	2	Q5TYT7_BRARE
18	332	10.6	637	2	Q6A073_MOUSE
19	331.5	10.6	622	2	Q59GV4_HUMAN
20	330	10.5	653	1	LRRC4_HUMAN
21	329.5	10.5	648	2	Q6DDY0_XENLA
22	325.5	10.4	570	2	Q70AK2_XENLA
23	324	10.3	626	1	LRFN3_MOUSE
24	324	10.3	626	2	Q505E2_MOUSE
25	323	10.3	732	2	Q4RPB8_TETNG
26	322.5	10.3	682	2	Q6DJD2_XENLA
27	322.5	10.3	811	2	Q7L0X0_HUMAN
28	322.5	10.3	887	2	Q75139_HUMAN
29	322	10.3	605	1	ALS_PAPHA
30	321	10.2	628	1	LRFN3_HUMAN
31	321	10.2	762	2	Q5JY13_HUMAN

32	320	10.2	660	1	FLRT2_HUMAN
33	320	10.2	674	2	Q6RKD8_MOUSE
34	319	10.2	602	2	Q58CS0_BOVIN
35	318.5	10.2	652	1	LRRC4_MOUSE
36	317	10.1	778	2	Q6NUI2_HUMAN
37	312.5	10.0	648	2	Q70AK3_XENLA
38	312.5	10.0	935	2	Q4SBT7_TETNG
39	311.5	9.9	420	2	Q7M6Z0_MOUSE
40	310.5	9.9	420	2	Q8OWD1_RAT
41	310.5	9.9	646	1	FLRT1_HUMAN
42	308	9.8	627	2	Q8NC95_HUMAN
43	308	9.8	649	1	FLRT3_HUMAN
44	308	9.8	649	2	Q542Z9_HUMAN
45	307.5	9.8	626	2	Q4TEM8_TETNG
46	307.5	9.8	674	2	Q8WVA2_HUMAN
47	307	9.8	637	2	Q68F21_XENLA
48	307	9.8	649	2	Q5R6T0_PONPY
49	306.5	9.8	730	2	Q6PHP6_MOUSE
50	305.5	9.7	730	2	Q6US92_MOUSE
51	303.5	9.7	692	2	Q4G0S0_HUMAN
52	302.5	9.6	420	2	Q6X813_HUMAN
53	302.5	9.6	420	2	Q86UN3_HUMAN
54	302.5	9.6	618	2	Q4SHD7_TETNG
55	302	9.6	605	1	ALS_HUMAN
56	302	9.6	605	2	Q8TAY0_HUMAN
57	299.5	9.6	677	2	Q28256_CANFA
58	298.5	9.5	649	2	Q8BGT1_MOUSE
59	298.5	9.5	663	2	Q6ZPQ1_MOUSE
60	295.5	9.4	640	1	NGLI1_MOUSE
61	295.5	9.4	640	2	Q505E5_MOUSE
62	294.5	9.4	640	2	Q50317_BRARE
63	293.5	9.4	809	2	Q9DBY4_MOUSE
64	292.5	9.3	640	1	NGLI1_HUMAN
65	292.5	9.3	837	2	Q80TV0_MOUSE
66	288.5	9.2	372	2	Q7F2W3_BRARE
67	288.5	9.2	581	2	Q4SY17_TETNG
68	288.5	9.2	640	2	Q4JIW0_HUMAN
69	287.5	9.2	428	2	Q4S4W6_TETNG
70	287.5	9.2	713	1	LRN5_HUMAN
71	286	9.1	650	2	Q4RQ15_TETNG
72	285	9.1	640	2	Q4JIV9_HUMAN
73	284.5	9.1	457	2	Q6WZD1_BRARE
74	284	9.1	782	2	Q5T0V4_HUMAN
75	283.5	9.0	603	2	Q70211_RAT
76	283	9.0	1515	2	Q9DE37_BRARE
77	282.5	9.0	745	2	Q6UXK2_HUMAN
78	282.5	9.0	785	2	Q9P263_HUMAN
79	282	9.0	626	1	GPIBA_HUMAN
80	281.5	9.0	603	1	ALS_RAT
81	281	9.0	738	2	Q90Z45_CHICK
82	280	8.9	633	2	Q4SR95_TETNG
83	279.5	8.9	619	2	Q570Z8_MOUSE
84	278.5	8.9	603	1	ALS_MOUSE
85	278.5	8.9	603	2	Q791Q5_MOUSE
86	278.5	8.9	321	2	Q79JL0_MOUSE
87	278	8.9	687	2	Q6B4K4_PETMA
88	278	8.9	1531	1	SLIT1_RAT
89	277	8.8	330	2	Q4G1K3_EPTBU
90	276	8.8	1071	2	Q4RTI6_TETNG
91	276	8.8	1531	1	SLIT1_MOUSE
92	276	8.8	2623	2	Q6WRI0_HUMAN
93	273.5	8.7	593	2	Q6UY18_HUMAN
94	273.5	8.7	1504	1	SLIT1_DROME
95	273	8.7	745	2	Q5RKR3_MOUSE
96	273	8.7	785	2	Q6ZPQ3_MOUSE
97	271.5	8.7	342	2	Q91X11_MOUSE
98	271.5	8.7	1312	2	Q61PFO_CAENRHABDI
99	271	8.6	473	1	RTN4R_HUMAN
100	271	8.6	473	1	RTN4R_MACFA
101	270.5	8.6	541	2	Q6PK41_HUMAN
102	270	8.6	478	2	Q6WZD2_BRARE
103	270	8.6	1461	2	Q5VW18_HUMAN
104	270	8.6	1534	1	SLIT1_HUMAN

Q43155	homo sapien
Q6rkd8	mus musculus
Q58c80	bos taurus
Q99ph1	mus musculus
Q6nu16	homo sapien
Q70ak3	xenopus lae
Q4sb7	tetradon n
Q7m6z0	mus musculus
Q8wd1	rattus norv
Q9nzul	homo sapien
Q8nc95	homo sapien
Q9nzul	homo sapien
Q542z9	homo sapien
Q4t8m8	tetradon n
Q8wva2	homo sapien
Q68f21	xenopus lae
Q5r6t0	pongo pygma
Q6ph6	mus musculus
Q6us92	mus musculus
Q4g0s0	homo sapien
Q6x813	homo sapien
Q86un3	homo sapien
Q4shd7	tetradon n
P35858	homo sapien
Q8t5y0	homo sapien
Q28256	canis famil
Q8bgt1	mus musculus
Q6zpg1	mus musculus
Q8c0j1	mus musculus
Q505e5	mus musculus
Q50317	brachydanio
Q9db4	m mus muscu
Q84w6	tetradon n
Q75325	homo sapien
Q4rq15	tetradon n
Q4jiv9	homo sapien
Q6wzd1	brachydanio
Q5t0v4	homo sapien
Q70211	rattus norv
Q9de37	brachydanio
Q6uxk2	homo sapien
Q9p263	homo sapien
P07359	homo sapien
P35859	rattus norv
Q90z45	gallus gall
Q4sr95	tetradon n
Q570z8	mus musculus
P70389	mus musculus
Q791q5	mus musculus
Q9jil0	mus musculus
Q6e4k4	petromyzon
Q82779	rattus norv
Q4g1k3	eptatretus
Q4rti6	tetradon n
Q80lr4	mus musculus
Q6wri0	homo sapien
Q6uy18	homo sapien
P24014	drosophila
Q5rkr3	mus musculus
Q6zpg3	mus musculus
Q91x11	mus musculus
Q61pfo	caenorhabdi
Q9bzr6	homo sapien
Q9n0e3	macaca fasc
Q6pk41	homo sapien
Q6wzd2	brachydanio
Q5vwl8	homo sapien
Q75093	homo sapien

105	270	8.6	1534	2	Q5VW17_HUMAN	Q5VW17 homo sapien
106	268.5	8.6	409	2	Q5T0V2_HUMAN	Q5T0V2 homo sapien
107	268	8.5	417	2	Q6E4J7_PETMA	Q6E4J7 petromyzon
108	267.5	8.5	1512	2	Q9DE36_BRARE	Q9DE36 brachydanio
109	266.5	8.5	1529	2	Q7ZX12_XENLA	Q7ZX12 xenopus lae
110	266	8.5	460	2	Q61PL6_HUMAN	Q61PL6 homo sapien
111	266	8.5	734	2	Q3S930_MOUSE	Q3S930 mus musculus
112	265.5	8.5	1044	2	Q5ISr9_MACFA	Q5ISr9 macaca fasc
113	265	8.4	298	2	Q4GL17_EPTBU	Q4GL17 eptatretus
114	265	8.5	734	2	Q5X47_MOUSE	Q5X47 mus musculus
115	264.5	8.4	420	1	TPBG_HUMAN	Q13641 homo sapien
116	264	8.4	334	2	Q5VSG2_HUMAN	Q5VSG2 homo sapien
117	264	8.4	352	2	Q4GL11_EPTBU	Q4GL11 eptatretus
118	263	8.4	332	2	Q5IOE3_RAT	Q5IOE1 rattus norv
119	263	8.4	1253	2	Q4T0S1_TETNG	Q4T0S1 tetraodon n
120	262	8.4	346	2	Q4GL19_EPTBU	Q4GL19 eptatretus
121	261.5	8.3	347	1	A2GL_HUMAN	P03750 homo sapien
122	261	8.3	1523	1	SLIT3_RAT	Q88280 rattus norv
123	258	8.2	321	2	Q6E4D1_PETMA	Q6E4D1 petromyzon
124	258	8.2	1223	1	SLIT3_HUMAN	Q75094 homo sapien
125	257.5	8.2	324	2	Q4S3K9_TETNG	Q4S3K9 tetraodon n
126	257.5	8.2	501	2	Q4SZC5_TETNG	Q4SZC5 tetraodon n
127	257	8.2	473	1	RTN4R_RAT	Q99m75 rattus norv
128	257	8.2	739	2	Q8BKM5_MOUSE	Q8BKM5 mus musculus
129	256.5	8.2	342	2	Q4S6G5_TETNG	Q4S6G5 tetraodon n
130	255.5	8.1	1095	2	Q90XG4_CHICK	Q90XG4 gallus gall
131	254	8.1	528	2	Q8N644_HUMAN	Q8N644 homo sapien
132	254	8.1	1523	1	SLIT3_MOUSE	Q9WVb4 mus musculus
133	254	8.1	1523	2	Q5S856_MOUSE	Q5S856 mus musculus
134	253.5	8.1	347	2	Q68CK4_HUMAN	Q68CK4 homo sapien
135	253.5	8.1	589	2	Q6GQU6_MOUSE	Q6GQU6 mus musculus
136	253.5	8.1	1410	2	Q20204_CABEL	Q20204 caenorhabdi
137	253	8.1	426	1	TPBG_MOUSE	Q08742 mus musculus
138	253	8.1	567	1	GPV_MOUSE	Q08741 petromyzon
139	252	8.0	311	2	Q64L1_PETMA	Q64L1 petromyzon
140	252	8.0	426	1	TPBG_RAT	Q5PGV5 rattus norv
141	252	8.0	567	2	Q9QZU3_MOUSE	Q9QZU3 mus musculus
142	251	8.0	473	1	RTN4R_MOUSE	Q99P18 mus musculus
143	251	8.0	542	2	Q9N4G6_CABEL	Q9N4G6 caenorhabdi
144	251	8.0	622	2	Q6ZW15_HUMAN	Q6ZW15 homo sapien
145	251	8.0	622	2	Q72Q07_HUMAN	Q72Q07 homo sapien
146	251	8.0	1021	2	Q9V430_DROME	Q9V430 drosophila
147	250	8.0	412	2	Q4RRU8_TETNG	Q4RRU8 tetraodon n
148	249.5	8.0	789	1	LRFN2_HUMAN	Q9ULh4 homo sapien
149	249.5	8.0	789	1	LRFN2_MACFA	Q9BE71 macaca fasc
150	249.5	8.0	297	2	Q6WRH9_RAT	Q6WRH9 rattus norv
151	248.5	7.9	420	1	TPBG_MACFA	Q4X8Y9 macaca fasc
152	248	7.9	481	1	NYX_HUMAN	Q9GZU5 homo sapien
153	248	7.9	481	2	Q5H983_HUMAN	Q5H983 homo sapien
154	247.5	7.9	305	2	Q4GL13_EPTBU	Q4GL13 eptatretus
155	247.5	7.9	1521	1	SLIT2_MOUSE	Q9R1B9 mus musculus
156	247.5	7.9	1529	1	SLIT2_HUMAN	Q94813 homo sapien
157	247.5	7.9	1530	2	Q90WZ3_XENLA	Q90WZ3 xenopus lae
158	247	7.9	794	2	Q4SK16_TETNG	Q4SK16 tetraodon n
159	246	7.8	308	2	Q4GL13_EPTST	Q4GL13 eptatretus
160	245.5	7.8	334	2	Q91W20_MOUSE	Q91W20 mus musculus
161	245.5	7.8	544	2	Q61X58_CABBR	Q61X58 caenorhabdi
162	245	7.8	306	2	Q4G1K6_EPTST	Q4G1K6 eptatretus
163	245	7.8	321	2	Q6E4J9_PETMA	Q6E4J9 petromyzon
164	245	7.8	708	2	Q81YQ6_HUMAN	Q81YQ6 homo sapien
165	245	7.8	708	2	Q5R482_PONPY	Q5R482 pongo pygma
166	244.5	7.8	411	2	Q4S6L6_TETNG	Q4S6L6 tetraodon n
167	244.5	7.8	718	2	SLIT2_RAT	Q73675 xenopus lae
168	244.5	7.8	766	1	SLIT2_MOUSE	Q9WVC1 rattus norv
169	244.5	7.8	788	1	LRFN2_MOUSE	Q80TG9 mus musculus
170	244.5	7.8	1593	2	Q5DTL5_MOUSE	Q5DTL5 mus musculus
171	244	7.8	458	2	Q6WZD3_BRARE	Q6WZD3 brachydanio
172	244	7.8	567	1	GPV_RAT	Q08770 rattus norv
173	244	7.8	708	2	Q9H3W5_HUMAN	Q9H3W5 homo sapien
174	243.5	7.8	476	1	NYX_MOUSE	P83503 mus musculus
175	243	7.8	321	2	Q64L4_PETMA	Q64L4 petromyzon
176	243	7.8	708	2	Q619V8_HUMAN	Q619V8 homo sapien
177	242.5	7.7	388	2	Q6ZM54_BRARE	Q6ZM54 brachydanio

178	242.5	7.7	545	1	CPN2_HUMAN	P22792 homo sapien
179	242.5	7.7	718	2	Q6PCK4_XENLA	Q6PCK4 xenopus lae
180	242	7.7	380	2	Q5T0V3_HUMAN	Q5T0V3 homo sapien
181	242	7.7	652	2	Q7PVZ3_ANOGA	Q7PVZ3 anopheles g
182	241.5	7.7	272	2	Q4K12_LAMAP	Q4K12 lampetra ap
183	241.5	7.7	311	2	Q6E4L3_PETMA	Q6E4L3 petromyzon
184	240	7.7	560	1	GPV_HUMAN	P40197 homo sapien
185	239.5	7.6	776	2	Q8BGX3_MOUSE	Q8BGX3 m mus muscu
186	239.5	7.6	370	2	Q5TU01_ANOGA	Q5TU01 anopheles g
187	239.5	7.6	786	2	Q7QCT2_ANOGA	Q7QCT2 anopheles g
188	238	7.6	1256	2	Q4KP13_9PETR	Q4KP13 ichtthyomyzo
189	238	7.6	453	2	Q86XV1_HUMAN	Q86XV1 homo sapien
190	238	7.6	544	2	Q8UV23_9PERC	Q8UV23 spherooides
191	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9D3K0 m mus muscu
192	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4S4C0 tetraodon n
193	237	7.6	289	2	Q4KP06_LAMAP	Q4KP06 lampetra ap
194	237	7.6	370	2	Q8N967_HUMAN	Q8N967 homo sapien
195	237	7.6	578	1	LRCL15_RAT	Q8r5m3 rattus norv
196	237	7.6	707	2	Q9ESY6_RAT	Q9ESY6 rattus norv
197	237	7.6	1046	2	Q7FZJ7_ANOGA	Q7FZJ7 anopheles g
198	236.5	7.5	461	2	Q4SA12_TETNG	Q4SA12 tetraodon n
199	236.5	7.5	715	2	Q4RY04_TETNG	Q4RY04 tetraodon n
200	236	7.5	707	2	Q8CBC6_MOUSE	Q8CBC6 mus musculus
201	236	7.5	718	2	Q6P627_XENLA	Q6P627 xenopus lae
202	235.5	7.5	296	2	Q4G1H6_EPTST	Q4G1H6 eptatretus
203	235.5	7.5	579	1	LRCL15_MOUSE	Q80x72 mus musculus
204	235	7.5	574	2	Q4RRK5_TETNG	Q4RRK5 tetraodon n
205	234.5	7.5	488	2	Q4RK86_TETNG	Q4RK86 tetraodon n
206	234	7.5	707	2	P97860_MOUSE	P97860 mus musculus
207	233.5	7.4	298	2	Q6E4J4_PETMA	Q6E4J4 petromyzon
208	233.5	7.4	545	2	Q5R534_PONPY	Q5R534 pongo pygma
209	233	7.4	1316	2	Q9VQ25_DROME	Q9VQ25 drosophila
210	232	7.4	487	2	Q4SA13_TETNG	Q4SA13 tetraodon n
211	231.5	7.4	283	2	Q4G1H4_EPTST	Q4G1H4 eptatretus
212	231.5	7.4	840	1	SLIK6_MOUSE	Q8C110 mus musculus
213	231	7.4	294	2	Q5VT99_HUMAN	Q5VT99 homo sapien
214	231	7.4	547	1	CPN2_MOUSE	Q9DBB9 mus musculus
215	231	7.4	619	2	Q7QBW2_ANOGA	Q7QBW2 anopheles g
216	231	7.4	707	2	Q642B4_RAT	Q642B4 rattus norv
217	231	7.4	787	2	Q4SW26_TETNG	Q4SW26 tetraodon n
218	230.5	7.4	687	2	Q4SCX3_TETNG	Q4SCX3 tetraodon n
219	230	7.3	332	2	Q8QFN6_ELAOU	Q8QFN6 elaphe quad
220	230	7.3	332	2	Q8QFN7_ELAOU	Q8QFN7 elaphe quad
221	230	7.3	872	2	Q4SZ04_TETNG	Q4SZ04 tetraodon n
222	230	7.3	1229	2	Q4T780_TETNG	Q4T780 tetraodon n
223	229.5	7.3	828	2	Q8C8T7_MOUSE	Q8C8T7 mus musculus
224	229	7.3	581	1	LRCL15_HUMAN	Q8tf66 homo sapien
225	228.5	7.3	394	2	Q6E4L6_PETMA	Q6E4L6 petromyzon
226	228.5	7.3	341	2	Q6ZSA7_HUMAN	Q6ZSA7 homo sapien
227	228.5	7.3	342	2	Q4RRU5_TETNG	Q4RRU5 tetraodon n
228	228	7.3	310	2	Q4RRQ4_TETNG	Q4RRQ4 tetraodon n
229	228	7.3	838	2	Q4SPF9_TETNG	Q4SPF9 tetraodon n
230	227.5	7.3	356	2	Q8BXQ3_MOUSE	Q8BXQ3 mus muscu
231	227	7.2	326	2	Q4KLL3_RAT	Q4KLL3 rattus norv
232	227	7.2	783	2	Q90XG2_CHICK	Q90XG2 gallus gall
233	227	7.2	950	2	Q90Z44_CHICK	Q90Z44 gallus gall
234	226.5	7.2	283	2	Q4G111_EPTST	Q4G111 eptatretus
235	226.5	7.2	298	2	Q4KP15_9PETR	Q4KP15 ichtthyomyzo
236	226.5	7.2	299	2	Q4G119_EPTST	Q4G119 eptatretus
237	226.5	7.2	557	1	LG11_HUMAN	Q95970 homo sapien
238	226.5	7.2	719	1	LRPN5_HUMAN	Q96N16 homo sapien
239	226	7.2	321	2	Q4KP16_9PETR	Q4KP16 ichtthyomyzo
240	226	7.2	364	2	Q4SQ63_TETNG	Q4SQ63 tetraodon n
241	225.5	7.2	210	2	Q4SCF1_TETNG	Q4SCF1 tetraodon n
242	225.5	7.2	298	2	Q6E4J3_PETMA	Q6E4J3 petromyzon
243	223.5	7.1	283	2	Q4G1H8_EPTST	Q4G1H8 eptatretus
244	223.5	7.1	647	2	Q4S1N0_TETNG	Q4S1N0 tetraodon n
245	223	7.1	289	2	Q6E4C8_PETMA	Q6E4C8 petromyzon
246	223	7.1	349	2	Q4SH52_TETNG	Q4SH52 tetraodon n
247	222.5	7.1	413	2	Q64215_MOUSE	Q64215 mus musculus
248	222.5	7.1	557	1	LG11_RAT	Q8k4Y5 rattus norv
249	222.5	7.1	557	2	Q5R945_PONPY	Q5R945 pongo pygma
250	222.5	7.1	557	2	Q5FWN7_RAT	Q5FWN7 rattus norv

251	222.5	7.1	792	2	Q90243_CHICK	O90243_gallus_gall	324	209	6.7	358	2	Q5SUV4_MOUSE	Q5SUV4_mus_musculus
252	222	7.1	269	2	Q6B410_PETMA	O6E410_tetrazodon_n	325	209	6.7	391	1	Q4S8B7_TETNG	Q4S8B7_tetrazodon_n
253	222	7.1	348	2	Q95J38_MACFA	O95J38_macaca_fasc	326	209	6.7	1091	1	LRIG1_MOUSE	LRIG1_mus_musculus
254	222	7.1	722	2	Q5PU2_XENLA	O5PU2_xenopus_lae	327	208.5	6.7	350	2	Q5RH05_BRARE	Q5RH05_brachydanio
255	221.5	7.1	475	2	Q4T109_TETNG	O4T109_tetrazodon_n	328	208.5	6.7	382	1	PRELP_HUMAN	PRELP_homo_sapien
256	221.5	7.1	557	1	LG11_MOUSE	O9J111_mus_musculus	329	208.5	6.7	382	2	Q6FHG6_HUMAN	Q6FHG6_homo_sapien
257	221.5	7.1	719	1	LRFN5_MOUSE	O8BXA0_mus_musculus	330	208.5	6.7	382	2	Q6FG38_HUMAN	Q6FG38_homo_sapien
258	221.5	7.1	721	1	Q5DTH4_MOUSE	O5DTH4_mus_musculus	331	208.5	6.7	445	2	Q8K0S5_MOUSE	Q8K0S5_m_reticulon
259	221	7.1	1093	1	LRIG1_HUMAN	O96J41_homo_sapien	332	208.5	6.7	479	2	Q6X3Y5_BRARE	Q6X3Y5_brachydanio
260	220.5	7.0	210	2	Q6E4M1_PETMA	O6E4M1_petromyzon	333	208.5	6.7	518	1	LRTM4_HUMAN	LRTM4_homo_sapien
261	220.5	7.0	306	2	Q4KP04_LAMAP	O4KP04_lampetra_ap	334	208.5	6.7	518	2	Q4FZ98_HUMAN	Q4FZ98_homo_sapien
262	220.5	7.0	342	2	Q6B4K1_PETMA	O6E4K1_petromyzon	335	208.5	6.7	519	2	Q4KMX1_HUMAN	Q4KMX1_homo_sapien
263	220.5	7.0	342	2	Q4RM94_TETNG	O4RM94_tetrazodon_n	336	208.5	6.7	537	1	LG14_HUMAN	LG14_homo_sapien
264	220.5	7.0	515	1	LRM2_MOUSE	O8BG83_mus_musculus	337	208.5	6.7	590	2	Q9VKJ7_HUMAN	Q9VKJ7_homo_sapien
265	220.5	7.0	515	1	LRM2_MOUSE	O8C811_mus_musculus	338	208	6.6	649	2	Q9VK22_DROME	Q9VK22_drosophila
266	220.5	7.0	733	2	Q24250_DROME	O24250_drosophila	339	207.5	6.6	180	2	Q6B4F0_PETMA	Q6B4F0_petromyzon
267	220.5	7.0	841	1	SLIK6_HUMAN	O9H5Y7_homo_sapien	340	207.5	6.6	330	2	Q4S074_TETNG	Q4S074_tetrazodon_n
268	220	7.0	582	1	LRM3_MOUSE	O8B281_mus_musculus	341	207.5	6.6	518	2	Q6ZT31_HUMAN	Q6ZT31_homo_sapien
269	220	7.0	582	2	Q8BZA0_MOUSE	O8BZA0_mus_musculus	342	207.5	6.6	1329	1	GP124_MOUSE	GP124_mus_musculus
270	220	7.0	603	2	Q4S27_TETNG	O4S27_tetrazodon_n	343	207	6.6	313	2	Q5T9K5_HUMAN	Q5T9K5_homo_sapien
271	219.5	7.0	583	2	Q4SNQ0_TETNG	O4SNQ0_tetrazodon_n	344	207	6.6	313	2	Q8N7C0_HUMAN	Q8N7C0_homo_sapien
272	219	7.0	334	2	Q6P7C4_RAT	O6P7C4_rattus_norv	345	207	6.6	536	2	Q8P0D2_BRARE	Q8P0D2_brachydanio
273	218.5	7.0	359	2	Q6GTU0_HUMAN	O6GTU0_homo_sapien	346	207	6.6	613	2	Q50L44_CHICK	Q50L44_gallus_gall
274	218.5	7.0	618	1	LRC21_MOUSE	O8K099_mus_musculus	347	207	6.6	740	2	Q5JMW6_HUMAN	Q5JMW6_homo_sapien
275	217.5	6.9	288	2	Q8BR15_MOUSE	O8BR15_mus_musculus	348	207	6.6	4293	2	O08852_MOUSE	O08852_mus_musculus
276	217.5	6.9	615	2	Q4SL57_TETNG	O4SL57_tetrazodon_n	349	206.5	6.6	270	2	Q6B4K6_PETMA	Q6B4K6_petromyzon
277	217.5	6.9	695	2	Q4T1V8_TETNG	O4T1V8_tetrazodon_n	350	206.5	6.6	274	2	Q6B4B9_PETMA	Q6B4B9_petromyzon
278	217.5	6.9	1335	2	Q61OC7_CAEBR	O61OC7_caenorhabdi	351	206.5	6.6	274	2	Q6B4C1_PETMA	Q6B4C1_petromyzon
279	217	6.9	637	2	Q6DCV7_XENLA	O6DCV7_xenopus_lae	352	206.5	6.6	327	2	Q6B4L2_PETMA	Q6B4L2_petromyzon
280	216	6.9	283	2	Q6E4C7_PETMA	O6E4C7_petromyzon	353	206.5	6.6	294	2	Q5U4S7_XENLA	Q5U4S7_xenopus_lae
281	216	6.9	282	2	Q4G1I6_EPTST	O4G1I6_eptatretus	354	206.5	6.6	423	2	Q8ND46_HUMAN	Q8ND46_homo_sapien
282	216	6.9	514	2	Q4VXB1_MOUSE	O4VXB1_mus_musculus	355	206.5	6.6	614	2	Q9DLT0_MOUSE	Q9DLT0_mus_musculus
283	215.5	6.9	329	2	Q56NG5_CIOIN	O56NG5_ciona_intes	356	206	6.6	353	2	Q9UJX9_HUMAN	Q9UJX9_homo_sapien
284	215.5	6.9	331	1	PLIB_AKBL	O56NG5_ciona_intes	357	206	6.6	353	2	Q8UJX8_HUMAN	Q8UJX8_homo_sapien
285	215.5	6.9	612	2	Q4SKY9_TETNG	O4SKY9_tetrazodon_n	358	206	6.6	381	1	PRELP_BOVIN	PRELP_bos_taurus
286	215.5	6.9	737	2	Q9VU51_DROME	O9VU51_drosophila	359	206	6.6	428	2	O14498_HUMAN	O14498_homo_sapien
287	215	6.9	743	2	Q6P1M7_HUMAN	O6P1M7_homo_sapien	360	206	6.6	539	2	Q5TPW2_ANOGA	Q5TPW2_anopheles_g
288	214.5	6.8	429	2	Q56NG6_CIOIN	O56NG6_ciona_intes	361	206	6.6	606	2	Q8BZD4_MOUSE	Q8BZD4_m_mus_muscu
289	214.5	6.8	341	2	Q86UN2_HUMAN	O86UN2_homo_sapien	362	206	6.6	606	2	Q8BLC0_MOUSE	Q8BLC0_m_mus_muscu
290	214.5	6.8	716	1	LRRN1_HUMAN	O6UXK5_homo_sapien	363	206	6.6	738	2	Q5ULI7_DROME	Q5ULI7_drosophila
291	214.5	6.8	731	2	Q4T149_TETNG	O4T149_tetrazodon_n	364	206	6.6	1054	1	LRIG2_MOUSE	LRIG2_mus_musculus
292	214.5	6.8	1535	2	Q23991_DROME	Q23991_drosophila	365	206	6.6	1127	2	Q4TAT9_TETNG	Q4TAT9_tetrazodon_n
293	214	6.8	295	2	Q6E4C9_PETMA	O6E4C9_petromyzon	366	205.5	6.6	212	2	Q6B4H2_PETMA	Q6B4H2_petromyzon
294	214	6.8	516	1	LRM2_HUMAN	O43300_homo_sapien	367	205.5	6.6	479	2	Q6DH76_BRARE	Q6DH76_brachydanio
295	214	6.8	717	2	Q4SR34_TETNG	O4SR34_tetrazodon_n	368	205.5	6.6	492	2	Q9SKT6_MOUSE	Q9SKT6_mus_musculus
296	214	6.8	2828	2	Q9NR99_HUMAN	O9NR99_homo_sapien	369	205.5	6.6	590	1	LRM4_MOUSE	LRM4_mus_musculus
297	213.5	6.8	238	2	Q6E4J5_PETMA	O6E4J5_petromyzon	370	205	6.5	248	2	Q4G1K4_EPTST	Q4G1K4_eptatretus
298	213.5	6.8	273	2	Q4G1L2_EPTBU	O4G1L2_eptatretus	371	205	6.5	256	2	Q4G1L6_EPTBU	Q4G1L6_eptatretus
299	213.5	6.8	359	1	CHAD_HUMAN	O15335_homo_sapien	372	205	6.5	486	2	Q4RU74_TETNG	Q4RU74_tetrazodon_n
300	213.5	6.8	361	1	CHAD_BOVIN	Q27972_bos_taurus	373	205	6.5	614	2	Q5RDX4_PONPY	Q5RDX4_pongo_pygma
301	213	6.8	438	2	Q7TO96_RAT	Q7TG96_rattus_norv	374	205	6.5	614	2	Q9N008_MACFA	Q9N008_macaca_fasc
302	213	6.8	716	1	LRRN1_MOUSE	O61809_mus_musculus	375	205	6.5	620	2	Q96FES_HUMAN	Q96FES_homo_sapien
303	212.5	6.8	604	2	Q4SHE8_TETNG	O4SHE8_tetrazodon_n	376	205	6.5	740	1	CT075_HUMAN	CT075_homo_sapien
304	212	6.8	276	2	Q4G1J9_EPTST	O4G1J9_eptatretus	377	204.5	6.5	463	2	Q8C1V9_MOUSE	Q8C1V9_mus_musculus
305	212	6.8	445	2	Q80WD0_RAT	Q80WD0_rattus_norv	378	204	6.5	353	2	Q6QMY6_RAT	Q6QMY6_rattus_norv
306	212	6.8	918	2	Q7Q3F0_ANOGA	O7Q3F0_anopheles_g	379	204	6.5	1173	2	Q9V7J8_DROME	Q9V7J8_drosophila
307	211.5	6.7	192	2	Q6E4I9_PETMA	O6E4I9_petromyzon	380	204	6.5	1306	2	Q6F4S1_XENLA	Q6F4S1_xenopus_lae
308	211.5	6.7	270	2	Q5R712_PONPY	O5R712_pongo_pygma	381	203.5	6.5	845	2	Q6A1I3_HUMAN	Q6A1I3_homo_sapien
309	211.5	6.7	518	2	Q5R712_PONPY	O5R712_pongo_pygma	382	203.5	6.5	894	2	Q9VKG1_DROME	Q9VKG1_drosophila
310	211	6.7	187	2	Q6E4I2_PETMA	O6E4I2_petromyzon	383	203.5	6.5	1061	2	Q53ME4_ORYSA	Q53ME4_oryza_sativ
311	211	6.7	581	1	LRM3_HUMAN	O86VH5_homo_sapien	384	203.5	6.5	1065	1	LRIG2_HUMAN	LRIG2_homo_sapien
312	211	6.7	581	1	LRM3_MOUSE	O9B9P6_macaca_fasc	385	203	6.5	269	2	Q6B4B6_PETMA	Q6B4B6_petromyzon
313	210.5	6.7	257	2	Q4G1M3_EPTBU	O4G1M3_eptatretus	386	203	6.5	428	2	Q5NVQ6_PONPY	Q5NVQ6_pongo_pygma
314	210.5	6.7	321	2	Q6E4L5_PETMA	O6E4L5_petromyzon	387	203	6.5	602	2	Q4R3P6_MACFA	Q4R3P6_macaca_fasc
315	210.5	6.7	4303	1	PKDI_HUMAN	P98161_homo_sapien	388	203	6.5	703	2	Q4SLZ4_TETNG	Q4SLZ4_tetrazodon_n
316	210	6.7	358	1	CHAD_RAT	O70210_rattus_norv	389	203	6.5	1514	2	Q6NN49_DROME	Q6NN49_drosophila
317	210	6.7	1028	2	Q86SR7_PIG	O86SR7_sus_scrofa	390	203	6.5	1514	2	Q9NBK9_DROME	Q9NBK9_drosophila
318	209.5	6.7	214	2	Q6B4H0_PETMA	O6B4H0_petromyzon	391	203	6.5	1514	2	Q9VUN0_DROME	Q9VUN0_drosophila
319	209.5	6.7	533	2	Q5EST6_BOVIN	O5EST6_bos_taurus	392	202.5	6.5	259	2	Q4G1K1_EPTST	Q4G1K1_eptatretus
320	209	6.7	211	2	Q6E4I3_PETMA	O6E4I3_petromyzon	393	202.5	6.5	259	2	Q4G1H5_EPTST	Q4G1H5_eptatretus
321	209	6.7	257	2	Q6E4J6_PETMA	O6E4J6_petromyzon	394	202.5	6.5	274	2	Q6E4J2_PETMA	Q6E4J2_petromyzon
322	209	6.7	353	2	Q6UXK1_HUMAN	O6UXK1_homo_sapien	395	202.5	6.5	829	2	Q4RIG0_TETNG	Q4RIG0_tetrazodon_n
323	209	6.7	358	1	CHAD_MOUSE	O55226_mus_musculus	396	202	6.4	271	2	Q4KP11_LAMAP	Q4KP11_lampetra_ap

397	6.4	202	1117	2	Q5VQM7_ORYSA	Q5vqm7	oryza sativ	470	194	6.2	692	2	Q4RV46_TETNG	Q4rv46	tetraodon n
398	201.5	6.4	187	2	Q6E4D7_PETMA	Q6e4d7	petromyzon	471	194	6.2	836	2	Q9V9V6_DROME	Q9v9v6	drosophila
399	201.5	6.4	275	2	Q4GLJ5_EPTST	Q4glj5	epitretus	472	193.5	6.2	186	2	Q6E4H8_PETMA	Q6e4h8	petromyzon
400	201.5	6.4	372	2	Q8CBR6_MOUSE	Q8cbr6	mus musculus	473	193.5	6.2	270	2	Q4KP03_LAMAP	Q4kp03	lampetra ap
401	201.5	6.4	457	2	Q960D1_DROME	Q960d1	drosophila n	474	193.5	6.2	273	2	Q4G1M1_EPTBU	Q4g1m1	epitretus
402	201.5	6.4	524	2	Q4RG59_TETNG	Q4rg59	tetraodon n	475	193.5	6.2	377	1	PRELP_RAT	Q4g1m1	rattus norv
403	201.5	6.4	551	2	Q4RF95_TETNG	Q4rf95	tetraodon n	476	193.5	6.2	378	2	Q8CAZ9_MOUSE	Q8caz9	mus musculus
404	201.5	6.4	606	2	Q9BZ20_HUMAN	Q9bz20	homo sapien	477	193.5	6.2	421	2	Q9NT99_HUMAN	Q9nt99	homo sapien
405	201.5	6.4	892	2	P91644_DROME	P91644	drosophila	478	193.5	6.2	433	2	Q61DGT_DROME	Q61dgt	drosophila
406	201.5	6.4	1527	2	Q9VZZ4_DROME	Q9vzz4	drosophila	479	193.5	6.2	545	1	LG12_HUMAN	Q8n0v4	homo sapien
407	201	6.4	213	2	Q6E4H6_PETMA	Q6e4h6	petromyzon	480	193.5	6.2	574	2	Q60W68_CABER	Q60w68	caenorhabdi
408	201	6.4	218	2	Q6E4K9_PETMA	Q6e4k9	petromyzon	481	193.5	6.2	721	1	Y2082_MYCTU	Q10690	mycobacteri
409	201	6.4	336	2	Q4S8M5_TETNG	Q4s8m5	tetraodon n	482	193.5	6.2	721	2	Q7TZ24_MYCBO	Q7tz24	mycobacteri
410	201	6.4	354	2	Q4W655_MOUSE	Q4w655	mus musculus	483	193.5	6.2	893	2	Q96C25_HUMAN	Q96c25	homo sapien
411	201	6.4	430	2	Q5BFT20_HUMAN	Q5bft20	homo sapien	484	193.5	6.2	910	2	Q9HB75_HUMAN	Q9hb75	homo sapien
412	201	6.4	581	2	Q9BTR7_HUMAN	Q9btr7	homo sapien	485	193.5	6.2	977	1	SLIK3_HUMAN	Q94933	homo sapien
413	201	6.4	602	2	Q9H9A6_HUMAN	Q9h9a6	homo sapien	486	193	6.2	252	2	Q4G1L2_EPTST	Q4g1l2	epitretus
414	201	6.4	712	2	Q5BL20_BRARE	Q5bl20	brachydanio	487	193	6.2	497	2	Q4S2U8_TETNG	Q4s2u8	tetraodon n
415	200.5	6.4	845	1	SLIK2_HUMAN	Q9h156	homo sapien	488	193	6.2	540	2	Q9NK84_DROME	Q9nk84	drosophila
416	200	6.4	460	2	Q4RK03_TETNG	Q4rk03	tetraodon n	489	193	6.2	550	2	Q9VJN8_DROME	Q9vjn8	drosophila
417	200	6.4	616	2	Q58A95_CABEL	Q58a95	caenorhabdi	490	192.5	6.1	187	2	Q6E4D5_PETMA	Q6e4d5	petromyzon
418	200	6.4	653	2	Q02329_CABEL	Q02329	caenorhabdi	491	192.5	6.1	214	2	Q6E4G0_PETMA	Q6e4g0	petromyzon
419	199.5	6.4	227	2	Q4SP28_TETNG	Q4sp28	tetraodon n	492	192.5	6.1	259	2	Q4G1H7_EPTST	Q4g1h7	epitretus
420	199.5	6.4	261	2	Q4G1L4_EPTBU	Q4g1l4	epitretus	493	192.5	6.1	270	2	Q6E4K0_PETMA	Q6e4k0	petromyzon
421	199.5	6.4	622	2	Q66HV9_BRARE	Q66hv9	brachydanio	494	192.5	6.1	428	2	Q6GU68_MOUSE	Q6gu68	mus musculus
422	199	6.3	846	1	SLIK2_MOUSE	Q810c0	mus musculus	495	192.5	6.1	542	2	Q50D27_MOUSE	Q50d27	mus musculus
423	199	6.3	862	2	Q4SST3_TETNG	Q4sst3	tetraodon n	496	192.5	6.1	1093	2	Q23580_CABEL	Q23580	caenorhabdi
424	199	6.3	1328	2	Q21043_CABEL	Q21043	caenorhabdi	497	192.5	6.1	575	2	Q6HA06_CRAGI	Q6ha06	crassostrea
425	198.5	6.3	259	2	Q4G1J4_EPTST	Q4g1j4	epitretus	498	192	6.1	265	2	Q6E4K2_PETMA	Q6e4k2	petromyzon
426	198.5	6.3	320	2	Q6YN44_HUMAN	Q6yn44	homo sapien	499	192	6.1	273	2	Q6E4C5_PETMA	Q6e4c5	petromyzon
427	198.5	6.3	617	1	LRC2L1_RAT	Q9jmh2	rattus norv	500	192	6.1	548	1	LG13_MOUSE	Q8k406	mus musculus
428	198.5	6.3	741	2	Q4SWG9_TETNG	Q4swg9	tetraodon n	501	192	6.1	627	2	Q6UN14_LEICH	Q6un14	leishmania
429	198.5	6.3	873	2	Q7XR24_ORYSA	Q7xr24	oryza sativ	502	191.5	6.1	187	2	Q6E4I7_PETMA	Q6e4i7	petromyzon
430	198.5	6.3	1331	1	GP124_HUMAN	Q9vpe1	homo sapien	503	191.5	6.1	204	2	Q6E4J8_PETMA	Q6e4j8	petromyzon
431	198	6.3	363	2	Q7SYE5_BRARE	Q7syex5	brachydanio	504	191.5	6.1	915	2	Q9ERV7_MOUSE	Q9erv7	mus musculus
432	198	6.3	602	2	Q5RFE9_PONPY	Q5rfe9	pongo pygma	505	191.5	6.1	980	1	SLIK3_MOUSE	Q810b9	mus musculus
433	197.5	6.3	280	2	Q6E4K3_PETMA	Q6e4k3	petromyzon	506	191.5	6.1	980	2	Q6NZM5_MOUSE	Q6nzm5	mus musculus
434	197.5	6.3	300	2	Q6E4K8_PETMA	Q6e4k8	petromyzon	507	191	6.1	271	2	Q4KP00_LAMAP	Q4kp00	lampetra ap
435	197.5	6.3	441	2	Q4VBZ3_HUMAN	Q4vzb3	homo sapien	508	191	6.1	440	2	Q5RC08_PONPY	Q5rcq8	pongo pygma
436	197.5	6.3	537	2	Q9VE49_DROME	Q9ve49	drosophila	509	191	6.1	610	2	Q4T1M0_TETNG	Q4t1m0	tetraodon n
437	197.5	6.3	548	1	LG13_HUMAN	Q8n145	homo sapien	510	190.5	6.1	251	2	Q4G1I7_EPTST	Q4g1i7	epitretus
438	197.5	6.3	548	1	Q4R4H3_MACFA	Q4r4h3	macaca fasc	511	190.5	6.1	894	2	Q5H721_FUGRU	Q5h721	fugu rubrip
439	197.5	6.3	818	2	Q4SIX2_TETNG	Q4six2	tetraodon n	512	190.5	6.1	1238	2	Q6NR19_DROME	Q6nr19	drosophila
440	197.5	6.3	835	2	Q4SFBO_TETNG	Q4sfbo	tetraodon n	513	190.5	6.1	1535	2	Q9VPF0_DROME	Q9vpf0	drosophila
441	197.5	6.3	1321	1	GP125_HUMAN	Q81wk6	homo sapien	514	190	6.1	191	2	Q6E4H3_PETMA	Q6e4h3	petromyzon
442	197	6.3	345	2	Q9HBL6_HUMAN	Q9hbl6	homo sapien	515	190	6.1	639	2	Q4RE68_TETNG	Q4re68	tetraodon n
443	197	6.3	694	2	Q6YXX5_ORYSA	Q6yxx5	oryza sativ	516	190	6.1	654	2	Q6Z8N6_CABER	Q6z8n6	caenorhabdi
444	197	6.3	1093	2	Q5XWD3_HUMAN	Q5xwd3	homo sapien	517	190	6.1	733	1	CT075_MOUSE	P59383	mus musculus
445	196.5	6.3	259	2	Q4G1J3_EPTST	Q4g1j3	epitretus	518	190	6.1	1119	1	LAIG3_HUMAN	Q6uxm1	homo sapien
446	196.5	6.3	261	2	Q4G1J7_EPTST	Q4g1j7	epitretus	519	190	6.1	1346	2	Q9V477_DROME	Q9v477	drosophila
447	196	6.3	263	2	Q6E4D0_PETMA	Q6e4d0	petromyzon	520	190	6.1	2800	2	Q6XHB1_DICDI	Q6xnb1	dictyostei
448	196	6.3	3638	2	Q15142_HUMAN	Q15142	homo sapien	521	189.5	6.0	252	2	Q4G1J7_EPTST	Q4g1j7	epitretus
449	195.5	6.2	370	2	Q58DI7_BOVIN	Q58di7	bos taurus	522	189.5	6.0	370	2	Q4RSX9_TETNG	Q4rsx9	tetraodon n
450	195.5	6.2	378	1	PRELP_MOUSE	Q91k53	mus musculus	523	189	6.0	369	1	PGS1_MOUSE	P28653	mus musculus
451	195.5	6.2	378	2	Q543S0_MOUSE	Q543s0	mus musculus	524	189	6.0	369	1	PGS1_RAT	P47853	rattus norv
452	195.5	6.2	917	2	Q86PM1_DROME	Q86pm1	drosophila	525	189	6.0	627	2	Q4TSR5_TETNG	Q4tsr5	tetraodon n
453	195.5	6.2	931	2	Q9VM16_DROME	Q9vpm1	drosophila	526	189	6.0	760	2	Q4QGI8_LEIMA	Q4ggi8	leishmania
454	195	6.2	440	2	Q4R5H2_MACFA	Q4r5h2	macaca fasc	527	189	6.0	839	2	Q9SN46_ARATH	Q9sn46	arabidopsis
455	195	6.2	614	2	Q6NUK3_HUMAN	Q6nuk3	homo sapien	528	189	6.0	1392	2	Q9VADI_DROME	Q9vad1	drosophila
456	195	6.2	620	2	Q6UXM3_HUMAN	Q6uxm3	homo sapien	529	189	6.0	4311	2	Q7YOK5_CANFA	Q7yok5	canis fami
457	195	6.2	837	1	SLIK4_HUMAN	Q81w52	homo sapien	530	188.5	6.0	369	2	Q6GM15_BRARE	Q6gm15	brachydanio
458	195	6.2	837	2	Q5UXG3_HUMAN	Q51xg3	homo sapien	531	188.5	6.0	370	2	Q504E0_BRARE	Q504e0	brachydanio
459	194.5	6.2	369	2	Q65Z91_CHICK	Q65z91	gallus gall	532	188.5	6.0	410	2	Q9DD27_PETMA	Q9dd27	petromyzon
460	194.5	6.2	693	2	Q7Z3D0_HUMAN	Q7z3d0	homo sapien	533	188.5	6.0	433	2	Q5SYH5_MOUSE	Q5syh5	mus musculus
461	194.5	6.2	699	1	ECM2_HUMAN	Q94769	homo sapien	534	188.5	6.0	440	1	OMGP_MOUSE	Q63912	mus musculus
462	194.5	6.2	699	2	Q5T9F2_HUMAN	Q5t9f2	homo sapien	535	188.5	6.0	538	2	Q5Z8W0_ORYSA	Q5z8w0	oryza sativ
463	194.5	6.2	737	2	Q965M3_CABEL	Q965m3	caenorhabdi	536	188.5	6.0	655	2	Q4SBU9_TETNG	Q4sbu9	tetraodon n
464	194.5	6.2	881	2	Q965M2_CABEL	Q965m2	caenorhabdi	537	188	6.0	368	2	Q53HU6_HUMAN	Q53hu6	homo sapien
465	194.5	6.2	1630	1	LAP4_HUMAN	Q14160	homo sapien	538	188	6.0	369	1	PGS1_CANFA	O02678	canis fami
466	194	6.2	258	2	Q4G1J0_EPTST	Q4g1j0	epitretus	539	188	6.0	369	2	Q7TWM3_MOUSE	Q7tmw3	mus musculus
467	194	6.2	258	2	Q4G1I0_EPTST	Q4g1i0	epitretus	540	188	6.0	522	1	LRTM1_MOUSE	Q8k377	mus musculus
468	194	6.2	263	2	Q6B4C0_PETMA	Q6e4c0	petromyzon	541	188	6.0	626	2	Q4SE92_TETNG	Q4se92	tetraodon n
469	194	6.2	611	2	Q4RHK3_TETNG	Q4rhk3	tetraodon n	542	188	6.0	818	2	Q5ZIH8_CHICK	Q5zih8	gallus gall

543	187.5	6.0	259	2	Q4G1L0_EPTBU	Q4g1l0 eptatretus	616	183	5.8	568	2	Q6P3Y9_MOUSE	Q6p3y9 mus musculus
544	187.5	6.0	310	2	Q9DDZ8_PETMA	Q9ddz8 petromyzon	617	183	5.8	662	1	LRC32_HUMAN	Lrc32 homo sapien
545	187.5	6.0	350	2	Q5M7S9_XENTR	Q5m7s9 xenopus tro	618	183	5.8	664	2	Q7ZT81_ONCMY	Q7zt81 oncorhynchus
546	187.5	6.0	352	2	Q4W6V7_CHICK	Q4w6v7 gallus gall	619	183	5.8	672	2	Q5ZJ34_CHICK	Q5zj34 gallus gall
547	187.5	6.0	363	2	Q9H5G9_HUMAN	Q9h5g9 homo sapien	620	182.5	5.8	672	2	Q6E4G3_PETMA	Q6e4g3 petromyzon
548	187.5	6.0	435	2	Q9VGH2_DROME	Q9vgh2 drosophila	621	182.5	5.8	187	2	Q6E4G7_PETMA	Q6e4g7 petromyzon
549	187.5	6.0	601	2	Q7SXW3_BRARE	Q7sxw3 brachydanio	622	182.5	5.8	257	2	Q4G1L8_EPTBU	Q4g1l8 eptatretus
550	187.5	6.0	861	2	Q4ZJ82_CHICK	Q4zj82 gallus gall	623	182.5	5.8	379	1	ASPN_HUMAN	Q9bxn1 homo sapien
551	187	6.0	260	2	Q4G1K7_EPTST	Q4g1k7 eptatretus	624	182.5	5.8	380	2	Q5TBF3_HUMAN	Q5tbf3 homo sapien
552	187	6.0	262	2	Q4G1K0_EPTST	Q4g1k0 eptatretus	625	182.5	5.8	384	2	Q6P528_HUMAN	Q6p528 homo sapien
553	187	6.0	592	2	Q61PG4_CABER	Q61pg4 caenorhabdi	626	182.5	5.8	810	2	Q8T3J2_DROME	Q8t3j2 drosophila
554	187	6.0	615	2	Q9VZ84_DROME	Q9vz84 drosophila	627	182.5	5.8	811	2	Q9VK54_DROME	Q9vk54 drosophila
555	187	6.0	735	2	Q6E1I4_MOUSE	Q6e1i4 mus musculus	628	182.5	5.8	828	1	TLR4_PONPY	Q8sep8 pongo pygma
556	187	6.0	818	2	Q5WAS1_CHICK	Q5was1 gallus gall	629	182.5	5.8	837	1	TLR4_GORGO	P91643 drosophila
557	187	6.0	1741	2	Q5WJ22_DROME	Q5wj22 drosophila	630	182.5	5.8	880	2	P91643_DROME	P91643 drosophila
558	186.5	5.9	368	1	PGS1_XENLA	Q9ib75 xenopus lae	631	182.5	5.8	958	1	SLIK5_HUMAN	Q94991 homo sapien
559	186.5	5.9	521	2	Q72U34_LEPIC	Q72u34 leptospira	632	182.5	5.8	958	2	Q5VT81_HUMAN	Q5vt81 homo sapien
560	186.5	5.9	639	2	Q5VZ17_HUMAN	Q5vz17 homo sapien	633	182.5	5.8	958	2	Q4QOH1_HUMAN	Q4qoh1 homo sapien
561	186.5	5.9	799	2	Q5VZ18_HUMAN	Q5vz18 homo sapien	634	182	5.8	205	2	Q4R9X7_TETNG	Q4r9x7 tetraodon n
562	186.5	5.9	839	1	Q5VZ18_HUMAN	Q5vz18 homo sapien	635	182	5.8	252	2	Q4G1I8_EPTST	Q4g1i8 eptatretus
563	186.5	5.9	839	1	TLR4_PANPA	Q9ttn0 pan paniscu	636	182	5.8	271	2	Q6E4C4_PETMA	Q6e4c4 petromyzon
564	186.5	5.9	839	2	Q5VZ19_HUMAN	Q5vz19 homo sapien	637	182	5.8	297	2	Q4RU73_TETNG	Q4ru73 tetraodon n
565	186	5.9	273	2	Q6E4B4_PETMA	Q6e4b4 petromyzon	638	182	5.8	369	1	PGS1_SHEEP	Q46390 ovis aries
566	186	5.9	368	2	Q5RAY4_PONPY	Q5ray4 pongo pygma	639	182	5.8	369	2	Q5BIM3_BOVIN	Q5bim3 bos taurus
567	186	5.9	440	1	OMG3_HUMAN	P23315 mus musculus	640	182	5.8	373	2	Q803T1_BRARE	Q803t1 brachydanio
568	186	5.9	440	2	Q53HB8_HUMAN	Q53hb8 homo sapien	641	182	5.8	373	2	Q5RI45_BRARE	Q5ri45 brachydanio
569	186	5.9	552	2	Q9VT44_DROME	Q9vt44 drosophila	642	182	5.8	428	2	Q8P3F8_LEPIN	Q8f3f8 leptospira
570	186	5.9	623	1	LRC21_HUMAN	Q9p2v4 homo sapien	643	182	5.8	532	2	Q96671_DROME	Q96671 drosophila
571	186	5.9	1029	2	Q512M5_BOVIN	Q512m5 bos taurus	644	182	5.8	678	2	Q7Q550_ANOGA	Q7q550 anopheles g
572	185.5	5.9	369	2	Q4T3M1_TETNG	Q4t3m1 tetraodon n	645	182	5.8	1022	2	Q8HXV0_BOVIN	Q8hvx0 bos taurus
573	185.5	5.9	466	2	Q661W3_XENLA	Q661w3 xenopus lae	646	182	5.8	1029	2	Q866B2_BOVIN	Q866b2 bos taurus
574	185.5	5.9	953	2	Q6MF87_PARUM	Q6mf87 parachlamyd	647	181.5	5.8	180	2	Q8BPJ0_MOUSE	Q8bpj0 mus musculus
575	185	5.9	254	2	Q4S4N7_TETNG	Q4s4n7 tetraodon n	648	181.5	5.8	251	2	Q4G1K2_EPTST	Q4g1k2 eptatretus
576	185	5.9	389	2	Q6BP55_BRARE	Q6bp55 brachydanio	649	181.5	5.8	259	2	Q4G1J8_EPTST	Q4g1j8 eptatretus
577	185	5.9	512	2	Q6PEZ8_HUMAN	Q6pez8 homo sapien	650	181.5	5.8	357	1	PGS2_CHICK	P28675 gallus gall
578	185	5.9	603	2	Q5ZLN0_CHICK	Q5zln0 gallus gall	651	181.5	5.8	599	2	Q7T3H6_BRARE	Q7t3h6 brachydanio
579	184.5	5.9	257	2	Q4G1L5_EPTBU	Q4g1l5 eptatretus	652	181.5	5.8	699	2	Q61PG3_CABER	Q61pg3 caenorhabdi
580	184.5	5.9	270	2	Q5XWB9_LAMAP	Q5xwb9 lampetra ap	653	181.5	5.8	2160	2	O13328_MAGGR	O13328 magnaporthe
581	184.5	5.9	724	2	Q5XWB9_HORSE	Q5xwb9 equus cabal	654	181.5	5.8	2160	2	O13488_MAGGR	O13488 magnaporthe
582	184.5	5.9	799	2	Q9V964_DROME	Q9v964 drosophila	655	181.5	5.8	2160	2	Q51J05_MAGGR	Q51j05 magnaporthe
583	184.5	5.9	839	2	Q69ZV6_MOUSE	Q69zv6 mus musculus	656	181	5.8	372	1	PGS1_HORSE	Q46403 equus cabal
584	184.5	5.9	841	2	Q5F4K7_PIG	Q5f4k7 sus scrofa	657	181	5.8	569	2	Q7QIP3_ANOGA	Q7qip3 anopheles g
585	184.5	5.9	843	1	TLR4_HORSE	Q9myw3 equus cabal	658	181	5.8	1013	2	Q8LQ10_ORYSA	Q8lq10 oryza sativ
586	184.5	5.9	957	1	SLIK5_MOUSE	Q810b7 mus musculus	659	181	5.8	1333	2	Q7Q168_ANOGA	Q7q168 anopheles g
587	184.5	5.9	957	2	SLIK5_MOUSE	Q65xs3 oryza sativ	660	180.5	5.8	371	2	Q6GLO6_XENLA	Q6gl06 xenopus lae
588	184.5	5.9	1007	2	Q65XS3_ORYSA	Q65xs3 gallus gall	661	180.5	5.8	385	2	Q8BMW6_MOUSE	Q8bmw6 mus musculus
589	184.5	5.9	1046	2	Q5G097_CHICK	Q5g097 gallus gall	662	180.5	5.8	441	2	Q81I70_DROVI	Q81i70 drosophila
590	184	5.9	1214	2	Q6JUN6_ORYSA	Q6jun6 oryza sativ	663	180.5	5.8	522	1	AMGO2_PONPY	Q5r7m3 pongo pygma
591	184	5.9	187	2	Q6E4M5_PETMA	Q6e4m5 petromyzon	664	180.5	5.8	584	2	Q6PGX3_BRARE	Q6pgx3 brachydanio
592	184	5.9	253	2	Q6E4K5_PETMA	Q6e4k5 petromyzon	665	180.5	5.8	821	2	Q9VPY3_HUMAN	Q9vp3 homo sapien
593	184	5.9	263	2	Q6E4K7_PETMA	Q6e4k7 petromyzon	666	180.5	5.8	1443	2	Q9VJQ0_HUMAN	Q9vjq0 drosophila
594	184	5.9	274	2	Q4G1M0_EPTBU	Q4g1m0 eptatretus	667	180.5	5.8	1460	2	Q5H261_XENTR	Q5h261 xenopus tro
595	184	5.9	291	2	Q4RF21_TETNG	Q4rf21 tetraodon n	668	180	5.7	250	2	Q4G1M2_EPTBU	Q4g1m2 eptatretus
596	184	5.9	368	1	PGS1_HUMAN	P21810 homo sapien	669	180	5.7	369	1	PGS1_BOVIN	P21809 bos taurus
597	184	5.9	368	2	Q53F14_HUMAN	Q53f14 homo sapien	670	180	5.7	522	1	LRTM1_PONPY	Q5t6b1 pongo pygma
598	184	5.9	473	2	Q7QF76_ANOGA	Q7qf76 anopheles g	671	180	5.7	817	2	Q86P15_DROME	Q86p15 drosophila
599	184	5.9	543	2	Q4RGC6_TETNG	Q4rgc6 tetraodon n	672	180	5.7	817	2	Q9VS84_DROME	Q9vs84 drosophila
600	184	5.9	552	2	Q6K6X6_ORYSA	Q6k6x6 oryza sativ	673	180	5.7	843	2	Q7ZTGS_CHICK	Q7ztgs gallus gall
601	184	5.9	565	2	Q7PJD0_ANOGA	Q7pjd0 anopheles g	674	180	5.7	869	2	Q4S0C1_TETNG	Q4s0c1 tetraodon n
602	183.5	5.9	837	1	SLIK4_MOUSE	Q810b8 mus musculus	675	179.5	5.7	187	2	Q6E4D6_PETMA	Q6e4d6 petromyzon
603	183.5	5.9	872	2	Q6E4F6_PETMA	Q6e4f6 petromyzon	676	179.5	5.7	585	2	Q61GX3_CABER	Q61gx3 caenorhabdi
604	183.5	5.9	287	2	Q9W2B9_DROME	Q9w2b9 drosophila	677	179.5	5.7	820	2	Q5R3F8_HUMAN	Q5r3f8 homo sapien
605	183.5	5.9	292	2	Q6NYT6_BRARE	Q6nyt6 brachydanio	678	179.5	5.7	1117	1	LRI3G_MOUSE	Q61c6 mus musculus
606	183.5	5.9	601	2	Q6TLH1_BRARE	Q6tlh1 brachydanio	679	179.5	5.7	4283	2	Q9ERV0_RAT	Q9erv0 rattus norv
607	183.5	5.9	652	2	Q7Q696_ANOGA	Q7q696 anopheles g	680	179	5.7	273	2	Q6E4B8_PETMA	Q6e4b8 petromyzon
608	183.5	5.9	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculus	681	179	5.7	314	2	Q5M8M9_MOUSE	Q5m8m9 mus musculus
609	183.5	5.9	795	1	TLR1_MOUSE	Q9epq1 mus musculus	682	179	5.7	534	2	Q9VT89_DROME	Q9vt89 drosophila
610	183.5	5.9	824	2	Q5GGX1_PIG	Q5ggx1 sus scrofa	683	179	5.7	700	2	Q9P244_HUMAN	Q9p244 homo sapien
611	183.5	5.9	841	1	TLR4_PIG	Q68y56 gallus gall	684	179	5.7	742	2	Q9BJD4_STRPU	Q9bjd4 strongyloce
612	183.5	5.9	1059	2	Q5ZJD0_CHICK	Q5zjd0 gallus gall	685	179	5.7	905	1	TLR3_MOUSE	Q99mb1 mus musculus
613	183.5	5.9	1495	2	Q5VXC2_HUMAN	Q5vxc2 homo sapien	686	179	5.7	969	2	Q4LBC9_ONCMY	Q4lbc9 oncorhynchus
614	183.5	5.9	1537	1	LRRC7_HUMAN	Q96nw7 homo sapien	687	179	5.7	1029	2	Q512M4_SHEEP	Q512m4 ovis aries
615	183	5.8	1537	2	Q5VXC3_HUMAN	Q5vxc3 homo sapien	688	178.5	5.7	176	2	Q567L5_BRARE	Q567l5 brachydanio
			540	2	Q9VU53_DROME	Q9vu53 drosophila							

689	178.5	5.7	190	2	Q6E4D8_PETMA	Q6E4d8	petromyzon	762	174.5	5.6	440	2	Q4J5V4_AZOVI	Q4j5v4	azotobacter
690	178.5	5.7	348	2	Q5R143_BRARE	Q5r143	brachydanio	763	174.5	5.6	512	2	Q3CQ76_MOUSE	Q3cq76	m mus muscu
691	178.5	5.7	356	1	PGS2_COTJA	Q9de68	coturnix co	764	174.5	5.6	567	2	Q4SLL10_TETNG	Q4sll10	tetraodon n
692	178.5	5.7	443	1	Q67VV7_ORYSA	Q67vv7	oryza sativ	765	174.5	5.6	602	2	Q3CRC8_MOUSE	Q3crc8	mus musculus
693	178.5	5.7	493	1	AMG01_HUMAN	Q86wk6	homo sapien	766	174.5	5.6	602	2	Q8BS83_MOUSE	Q8bs83	mus musculus
694	178.5	5.7	587	1	Q4OGJ9_LEIMA	Q4ggj9	leishmania	767	174.5	5.6	602	2	Q78WQ9_MOUSE	Q78wq9	mus musculus
695	178.5	5.7	1024	1	POPC_RALSO	Q9rba2	ralstonia s	768	174.5	5.6	605	2	Q6GPJ5_XENLA	Q6gpj5	xenopus lae
696	178.5	5.7	1063	2	Q5Z6G6_ORYSA	Q5z666	oryza sativ	769	174.5	5.6	795	1	TLR6_MOUSE	Q9epw9	mus musculus
697	178.5	5.7	1104	2	Q7XUH4_ORYSA	Q7xuh4	oryza sativ	770	174.5	5.6	1020	2	Q5ZED4_ORYSA	Q5zed4	oryza sativ
698	178.5	5.7	1310	1	GP125_MOUSE	Q7tt36	mus musculus	771	174.5	5.6	1060	2	Q6ZGM3_ORYSA	Q6zgm3	oryza sativ
699	178	5.7	187	2	Q6E4H4_PETMA	Q6e4h4	petromyzon	772	174	5.6	490	2	Q4RYL5_TETNG	Q4ryl5	tetraodon n
700	178	5.7	364	2	Q6GJ59_XENLA	Q6gj59	xenopus lae	773	174	5.6	535	2	Q8RX50_BRANI	Q8rx50	brassica ni
701	178	5.7	391	2	Q4FQI1_TETNG	Q4fqil	tetraodon n	774	174	5.6	544	2	Q7Q2W5_ANOGA	Q7qx25	anopheles g
702	178	5.7	488	2	Q4RXQ5_TETNG	Q4rxq5	tetraodon n	775	174	5.6	651	2	Q4JQQ2_XENLA	Q4jqd2	xenopus lae
703	178	5.7	522	1	LRTM1_HUMAN	Q86ue6	homo sapien	776	174	5.6	859	1	TLR5_MOUSE	Q9jlf7	mus musculus
704	178	5.7	894	2	Q9BJD6_STRPU	Q9bjd6	strongyloce	777	174	5.6	951	1	LGR4_RAT	Q9z2h4	rattus norv
705	178	5.7	1049	1	TLR7_HUMAN	Q9nyk1	homo sapien	778	173.5	5.5	261	2	Q5M8T1_HUMAN	Q5m8t1	homo sapien
706	178	5.7	1052	2	Q9Y4C4_HUMAN	Q9y4c4	homo sapien	779	173.5	5.5	337	2	Q4RJX0_TETNG	Q4rjx0	tetraodon n
707	178	5.7	1257	2	Q7PNF8_ANOGA	Q7pnf8	anopheles g	780	173.5	5.5	353	2	Q640B1_XENTR	Q640b1	xenopus tro
708	177.5	5.7	275	2	Q4G1K5_EPTST	Q4g1k5	epitaretus	781	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8	xenopus lae
709	177.5	5.7	796	2	Q59HI9_PIG	Q59hi9	sus scrofa	782	173.5	5.5	421	1	OMD_HUMAN	Q99983	homo sapien
710	177.5	5.7	796	2	Q4LDR7_PIG	Q4ldr7	sus scrofa	783	173.5	5.5	421	2	Q5TBF4_HUMAN	Q5tbf4	homo sapien
711	177.5	5.7	809	2	Q4RMO1_TETNG	Q4rmq1	tetraodon n	784	173.5	5.5	440	2	Q7TQ25_RAT	Q7tg25	rattus norv
712	177.5	5.7	1026	2	Q5SMW2_ORYSA	Q5smw2	oryza sativ	785	173.5	5.5	537	1	LG14_MOUSE	Q8k1s1	mus musculus
713	177.5	5.7	1050	1	TLR7_MOUSE	P58681	mus musculus	786	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21	bos taurus
714	177.5	5.7	1050	2	Q548J0_MOUSE	Q548j0	mus musculus	787	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7cp5	mus musculus
715	177.5	5.7	1360	2	Q7KTA0_DROME	Q7kta0	drosophila	788	173.5	5.5	826	1	TLR4_PAPAN	Q7esp2	papio anubi
716	177.5	5.7	1530	2	Q68D07_HUMAN	Q68d07	homo sapien	789	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720	fugu rubrip
717	177.5	5.7	2000	1	CYAA_NEUCR	P01631	neurospora	790	173	5.5	252	2	Q4G1I4_EPTST	Q4g1i4	epitaretus
718	177.5	5.7	2493	1	CYAA_USTMA	P49606	ustilago ma	791	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2	petromyzon
719	177.5	5.7	2493	2	Q4P3T1_USTMA	Q4p3t1	ustilago ma	792	173	5.5	360	1	PGS2_HORSE	Q46542	equus cabal
720	177	5.6	187	2	Q6E4H5_PETMA	Q6e4h5	petromyzon	793	173	5.5	470	2	Q9V354_DROME	Q9v354	drosophila
721	177	5.6	334	2	Q4SBU8_TETNG	Q4sbu8	tetraodon n	794	173	5.5	539	2	Q5O3F6_BRARE	Q5o3f6	brachydanio
722	177	5.6	343	1	LUM_COTJA	Q9de67	coturnix co	795	173	5.5	664	2	Q5UT54_SALSA	Q5ut54	salmo salar
723	177	5.6	347	2	Q58A48_BRARE	Q58a48	brachydanio	796	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40	mus musculus
724	177	5.6	662	2	Q5RF01_PONPY	Q5rf01	pongo pygma	797	173	5.5	925	1	GLHR_ATEL	P35409	anthopleura
725	177	5.6	666	2	Q7Q2M6_ANOGA	Q7q2w6	anopheles g	798	173	5.5	1459	2	Q7Q0C5_ANOGA	Q7q0c5	anopheles g
726	177	5.6	670	2	Q5FW85_MOUSE	Q5fw85	mus musculus	799	173	5.5	1459	2	Q8WR54_ANOGA	Q8wre4	anopheles g
727	177	5.6	1370	2	Q5BNA4_APIME	Q5bna4	apis mellif	800	172.5	5.5	163	2	Q6E4E2_PETMA	Q6e4e2	petromyzon
728	176.5	5.6	187	2	Q6E4M0_PETMA	Q6e4m0	petromyzon	801	172.5	5.5	353	1	KERA_CHICK	Q42335	gallus gall
729	176.5	5.6	520	2	Q5VR46_ORYSA	Q5vr46	oryza sativ	802	172.5	5.5	353	1	KERA_COTJA	P07585	homo sapien
730	176.5	5.6	522	1	AMG02_HUMAN	Q86sj2	homo sapien	803	172.5	5.5	359	1	PGS2_HUMAN	Q5r1v9	pan troglod
731	176.5	5.6	522	2	Q4VBP6_HUMAN	Q4vbp6	homo sapien	804	172.5	5.5	359	1	PGS2_PANTR	Q5r1v9	pan troglod
732	176.5	5.6	628	2	Q7PVZ6_ANOGA	Q7pvz6	anopheles g	805	172.5	5.5	359	2	Q6FH10_HUMAN	Q6fhl0	homo sapien
733	176.5	5.6	856	2	Q59HI7_PIG	Q59hi7	sus scrofa	806	172.5	5.5	378	2	Q5R294_DROSI	Q5r294	drosophila
734	176.5	5.6	934	1	Q4SBD4_TETNG	Q4sbda	tetraodon n	807	172.5	5.5	739	2	Q6ONV9_CAEBR	Q6onv9	caenorhabdi
735	176.5	5.6	1495	1	LRRCT_RAT	P70587	rattus norv	808	172.5	5.5	823	2	Q8CCW8_MOUSE	Q8ccw8	mus musculus
736	176.5	5.6	1756	2	Q6AWK6_DROME	Q6awk6	drosophila	809	172.5	5.5	823	2	Q68FM6_MOUSE	Q68fm6	mus musculus
737	176	5.6	249	2	Q4SDM4_TETNG	Q4sdm4	tetraodon n	810	172.5	5.5	1711	2	Q59DT7_DROME	Q59dt7	drosophila
738	176	5.6	503	2	Q8LJ87_ORYSA	Q8lj87	oryza sativ	811	172.5	5.5	1850	2	Q59DT8_DROME	Q59dt8	drosophila
739	176	5.6	623	2	Q95S21_DROME	Q95s21	drosophila	812	172.5	5.5	1851	1	LAP4_DROME	Q7kry7	drosophila
740	176	5.6	862	2	Q5GR02_CHICK	Q5gr02	gallus gall	813	172.5	5.5	4256	2	Q8MJF3_CANFA	Q8mjf3	canis faml
741	176	5.6	904	2	Q5TJ59_BOVIN	Q5tj59	bos taurus	814	172	5.5	339	2	Q4SU68_TETNG	Q4su68	tetraodon n
742	176	5.6	905	2	Q5TJ58_BOVIN	Q5tj58	bos taurus	815	172	5.5	347	2	Q7ZUT1_BRARE	Q7zut1	brachydanio
743	176	5.6	906	2	Q4SRZ0_TETNG	Q4srz0	tetraodon n	816	172	5.5	411	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
744	176	5.6	1032	2	Q5I2M8_DROME	Q5i2m8	canis faml	817	172	5.5	577	2	Q8N3K5_HUMAN	Q8n3k5	homo sapien
745	176	5.6	1257	2	Q9VK28_DROME	Q9vk28	drosophila	818	172	5.5	1134	2	Q65510_ARATH	Q65510	arabidopsis
746	176	5.6	1412	1	LAP2_HUMAN	Q96rt1	homo sapien	819	172	5.5	1693	2	Q4INH4_GIBZE	Q4inh4	gibberella
747	175.5	5.6	272	2	Q4KP14_9PETR	Q4kp14	ichthyomyzo	820	171.5	5.5	378	2	Q9V900_DROME	Q9v900	drosophila
748	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4	tetraodon n	821	171.5	5.5	605	2	Q5M8G4_XENTR	Q5m8g4	xenopus tro
749	175.5	5.6	440	2	Q7TNM3_RAT	Q7tnm3	rattus norv	822	171.5	5.5	683	1	LRCHA_HUMAN	Q75427	homo sapien
750	175.5	5.6	492	1	AMG01_MOUSE	Q80zd8	mus musculus	823	171.5	5.5	858	1	TLR5_HUMAN	Q60602	homo sapien
751	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718	fugu rubrip	824	171.5	5.5	858	2	Q5U308_RAT	Q5u308	rattus norv
752	175.5	5.6	1490	1	LRRCT_MOUSE	Q80te7	mus musculus	825	171.5	5.5	859	1	LRRCS_MOUSE	Q8bgr2	mus musculus
753	175.5	5.6	1731	2	Q4S0D3_TETNG	Q4s0d3	tetraodon n	826	171.5	5.5	1589	2	Q9UUQ9_METAN	Q9uud9	metarhizium
754	175	5.6	252	2	Q4GLJ2_EPTST	Q4glj2	epitaretus	827	171	5.5	360	1	PGS2_PIG	Q9xsd9	sus scrofa
755	175	5.6	343	1	LUM_CHICK	P51890	gallus gall	828	171	5.5	360	2	Q6DV11_GECJA	Q6dv11	gecko japon
756	175	5.6	429	2	Q8BJ09_MOUSE	Q8bj09	mus musculus	829	171	5.5	552	2	Q86V06_HUMAN	Q86v06	homo sapien
757	175	5.6	510	2	Q9BGY6_MACFA	Q9bgy6	macaca fasc	830	171	5.5	643	2	Q502J4_BRARE	Q502j4	brachydanio
758	175	5.6	941	2	Q5H722_FUGRU	Q5h722	fugu rubrip	831	171	5.5	833	1	TLR4_FELCA	P58727	felis silve
759	175	5.6	973	2	Q6KCC7_ONCMY	Q6kcc7	oncorhynch	832	171	5.5	1317	2	Q5TUS9_ANOGA	P58729	anopheles g
760	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1	anopheles g	833	170.5	5.4	246	2	Q6E4J1_PETMA	Q6e4j1	petromyzon
761	174.5	5.6	190	2	Q6E4E5_PETMA	Q6e4e5	petromyzon	834	170.5	5.4	359	2	Q4R5D2_MACFA	Q4r5d2	macaca fasc

835	170.5	5.4	373	1	ASPN_MOUSE	Q99mq4	mus musculus	908	167	5.3	1112	2	Q4G2W2_LYCPM	Q4g2w2 lycopersico
836	170.5	5.4	741	2	Q8KTF7_LISMO	Q8kcf7 listeria mo	909	167	5.3	1263	2	Q4SID1_TETNG	Q4sid1 tetraodon n	
837	170.5	5.4	1031	2	Q512M7_FELCA	Q512m7 felis silve	910	167	5.3	1845	2	Q5QNO9_MOUSE	Q5gnq9 mus musculus	
838	170.5	5.4	1031	2	Q8h252_FELCA	Q8h252 felis silve	911	166.5	5.3	163	2	Q6E4D4_PETMA	Q6e4d4 petromyzon	
839	170.5	5.4	2145	1	CYAA_PODAN	Q01513 podospora a	912	166.5	5.3	483	2	Q5NE36_LISMO	Q5ne36 listeria mo	
840	170	5.4	187	2	Q6E4D9_PETMA	Q6e4d9 petromyzon	913	166.5	5.3	549	2	Q9SVW8_ARATH	Q9svw8 arabidopsis	
841	170	5.4	364	1	LRCI19_MOUSE	Q8bzt5 mus musculus	914	166.5	5.3	582	2	Q5R423_PONPY	Q5r423 pongo pygma	
842	170	5.4	572	2	Q4QGJ6_LEIMA	Q4qgj6 leishmania	915	166.5	5.3	739	2	Q84CF6_LISMO	Q84cf6 listeria mo	
843	170	5.4	883	2	Q4VAM0_HUMAN	Q4vam0 homo sapien	916	166.5	5.3	741	2	Q8KTF0_LISMO	Q8kTf0 listeria mo	
844	170	5.4	907	1	LGR5_HUMAN	Q75473 homo sapien	917	166.5	5.3	741	2	Q8KTF9_LISMO	Q8kTf9 listeria mo	
845	170	5.4	1024	2	Q4VAM2_HUMAN	Q4vam2 homo sapien	918	166.5	5.3	743	2	Q95RV9_DROME	Q95rv9 drosophila	
846	170	5.4	1024	2	Q841E6_RALSO	Q841e6 ralstonia s	919	166.5	5.3	743	2	Q8KTF2_LISMO	Q8kTf2 listeria mo	
847	170	5.4	1032	2	Q59ER8_HUMAN	Q59er8 homo sapien	920	166.5	5.3	744	2	Q8KHNI_LISMO	Q8khni listeria mo	
848	170	5.4	1471	2	Q7KW92_DROME	Q7kw92 drosophila	921	166.5	5.3	744	2	Q8KTF1_LISMO	Q8kTf1 listeria mo	
849	169.5	5.4	352	1	KERA_BOVIN	Q62702 bos taurus	922	166.5	5.3	744	2	Q8KTF1_LISMO	Q8kTf1 listeria mo	
850	169.5	5.4	366	2	Q8BX06_MOUSE	Q8bx06 m mus muscu	923	166.5	5.3	744	2	Q8KTF5_LISMO	Q8kTf5 listeria mo	
851	169.5	5.4	493	1	AMEQ01_RAT	Q800d7 rattus norv	924	166.5	5.3	744	2	Q8KTF8_LISMO	Q8kTf8 listeria mo	
852	169.5	5.4	651	2	Q4T8T5_TETNG	Q4t8t9 tetraodon n	925	166.5	5.3	746	2	Q8KTF3_LISMO	Q8kTf3 listeria mo	
853	169.5	5.4	760	2	Q97OK5_ARATH	Q97ok5 arabidopsis	926	166.5	5.3	792	2	Q5NE37_LISMO	Q5ne37 listeria mo	
854	169.5	5.4	876	2	Q67WES_ORYSA	Q67wes oryza sativ	927	166.5	5.3	800	1	INLA_LISMF	Q723k6 listeria mo	
855	169.5	5.4	991	2	Q6R5N8_MOUSE	Q6r5n8 mus musculus	928	166.5	5.3	800	1	INLA_LISMO	P25146 listeria mo	
856	169.5	5.4	1271	1	FLII_MOUSE	Q91j28 mus musculus	929	166.5	5.3	1012	2	Q95YI6_ASTPE	Q95yi6 asterina pe	
857	169	5.4	217	2	Q66WJ6_FELCA	Q66wj6 felis silve	930	166.5	5.3	1115	2	Q652D9_ORYSA	Q652d9 oryza sativ	
858	169	5.4	273	2	Q5XPY6_ICTPU	Q5xpy6 ictalurus p	931	166.5	5.3	1215	2	Q60PY2_CABBR	Q60py2 caenorhabdi	
859	169	5.4	279	2	Q5QHK2_TRASC	Q5qhk2 trachemys s	932	166.5	5.3	1270	2	Q7QHP7_ANOGA	Q7qhp7 anopheles g	
860	169	5.4	354	1	PGS2_MOUSE	P28654 mus musculus	933	166.5	5.3	1280	2	Q95YI7_ASTPE	Q95yi7 asterina pe	
861	169	5.4	360	2	Q6J0Y6_PAROL	Q6j0y6 paralichthy	934	166.5	5.3	3204	2	Q6X248_9ALPH	Q6x248 bovine herp	
862	169	5.4	757	2	Q6RMS7_ORYSA	Q6rnm87 oryza sativ	935	166	5.3	163	2	Q6E4F8_PETMA	Q6e4f8 petromyzon	
863	169	5.4	839	2	Q9RKS7_DEIRA	Q9rx57 deinococcus	936	166	5.3	245	2	Q4KP01_LAWAP	Q4kp01 lampetra ap	
864	169	5.4	1175	2	Q4RER3_TETNG	Q4rer3 tetraodon n	937	166	5.3	426	2	Q72TC3_LEPIC	Q72tc3 leptospira	
865	169	5.4	1288	2	Q624K5_CABBR	Q624k5 caenorhabdi	938	166	5.3	768	2	Q4SSE3_TETNG	Q4sse3 tetraodon n	
866	169	5.4	1658	2	Q4PLE9_FUSPR	Q4ple9 fusarium pr	939	166	5.3	806	2	Q6P690_RAT	Q6p690 rattus norv	
867	168.5	5.4	246	2	Q4KP10_LAWAP	Q4kp10 lampetra ap	940	166	5.3	835	1	TLR4_RAT	Q9x05 rattus norv	
868	168.5	5.4	255	2	Q66WJ3_FELCA	Q66wj3 felis silve	941	166	5.3	1030	2	Q5I2M3_PIG	Q5i2m3 sus scrofa	
869	168.5	5.4	333	2	Q4SY28_TETNG	Q4sy28 tetraodon n	942	166	5.3	1030	2	Q8E5R8_PIG	Q8e5r8 sus scrofa	
870	168.5	5.4	343	2	Q501S3_BRARE	Q501s3 brachydanio	943	166	5.3	1110	2	Q7G768_ORYSA	Q7g768 oryza sativ	
871	168.5	5.4	353	2	Q7SYS8_XENLA	Q7sys8 xenopus lae	944	166	5.3	1110	2	Q94LN2_ORYSA	Q94ln2 oryza sativ	
872	168.5	5.4	363	2	Q8C8A7_MOUSE	Q8c8a7 mus musculus	945	166	5.3	1221	2	Q9N523_CABEL	Q9n523 caenorhabdi	
873	168.5	5.4	378	2	Q5R264_DROSE	Q5r264 drosophila	946	166	5.3	2139	2	Q4PDM0_USTMA	Q4pdw0 ustilago ma	
874	168.5	5.4	619	2	Q6X8K0_ORYSA	Q6x8k0 oryza sativ	947	165.5	5.3	327	2	Q5RHE5_BRARE	Q5rhe5 brachydanio	
875	168.5	5.4	685	2	Q6T545_LISMO	Q6t545 listeria mo	948	165.5	5.3	360	1	PGS2_BOVIN	P21793 bos taurus	
876	168.5	5.4	694	2	Q61P91_CABBR	Q61p91 caenorhabdi	949	165.5	5.3	360	1	PGS2_CANFA	P21793 canis fami	
877	168.5	5.4	728	2	Q6T546_LISMO	Q6t546 listeria mo	950	165.5	5.3	526	2	Q7XJ53_ARATH	Q7xj53 arabidopsis	
878	168.5	5.4	744	2	Q8KTF6_LISMO	Q8kTf6 listeria mo	951	165.5	5.3	641	2	Q5H716_FUGRU	Q5h716 fugu rubrip	
879	168.5	5.4	907	1	LGR5_MOUSE	Q921p4 mus musculus	952	165.5	5.3	1101	2	Q59H95_HUMAN	Q59h95 homo sapien	
880	168.5	5.4	1036	2	Q9FN37_ARATH	Q9fn37 arabidopsis	953	165.5	5.3	1256	1	FLII_DROME	Q24020 drosophila	
881	168.5	5.4	1360	2	Q9NDI1_DROME	Q9ndi1 drosophila	954	165.5	5.3	1269	1	FLII_HUMAN	Q13045 homo sapien	
882	168.5	5.4	1724	2	Q4H4B6_BRARE	Q4h4b6 brachydanio	955	165.5	5.3	1269	1	Q5R4G9_PONPY	Q5r4g9 pongo pygma	
883	168	5.4	351	2	Q65YW8_XENLA	Q65yw8 xenopus lae	956	165	5.3	1269	2	Q4RX02_TETNG	Q4rx02 tetraodon n	
884	168	5.4	402	2	Q72U35_LEPIC	Q72u35 leptospira	957	165	5.3	436	2	Q5R6F8_PONPY	Q5r6f8 pongo pygma	
885	168	5.4	753	2	Q9NRE6_HUMAN	Q9nre6 homo sapien	958	165	5.3	902	2	Q7RYP2_NEUCR	Q7ryp2 neurospora	
886	168	5.4	773	2	Q5NE35_LISMO	Q5ne35 listeria mo	959	165	5.3	994	2	Q9C637_ARATH	Q9c637 arabidopsis	
887	168	5.4	951	1	LGR4_HUMAN	Q9bxb1 homo sapien	960	165	5.3	1135	2	Q7XS12_ORYSA	Q7xs12 oryza sativ	
888	168	5.4	977	2	Q8GVW0_ORYSA	Q8gvw0 oryza sativ	961	165	5.3	1154	2	Q7QHH4_ANOGA	Q7qhh4 anopheles g	
889	167.5	5.3	147	2	Q9TTO0_PIG	Q9tt00 sus scrofa	962	164.5	5.2	235	2	Q4LVE2_9BURK	Q4lve2 eptaretus	
890	167.5	5.3	351	1	KERA_MOUSE	Q53367 mus musculus	963	164.5	5.2	468	2	Q4LVE2_9BURK	Q4lve2 burkholderi	
891	167.5	5.3	360	1	PGS2_SHEEP	Q9tte2 ovis aries	964	164.5	5.2	582	1	SHOC2_HUMAN	Q9uq13 homo sapien	
892	167.5	5.3	378	2	Q72U36_LEPIC	Q72u36 leptospira	965	164.5	5.2	582	2	Q5VZS9_HUMAN	Q5vzs9 homo sapien	
893	167.5	5.3	396	2	Q8C3D9_MOUSE	Q8c3d9 mus musculus	966	164.5	5.2	582	2	Q5RAV5_PONPY	Q5rav5 pongo pygma	
894	167.5	5.3	422	1	OMD_BOVIN	Q77742 bos taurus	967	164.5	5.2	734	2	Q5R7N1_PONPY	Q5r7n1 pongo pygma	
895	167.5	5.3	694	2	Q4RYL2_TETNG	Q4ryl2 tetraodon n	968	164.5	5.2	805	2	Q658W7_HUMAN	Q658w7 homo sapien	
896	167.5	5.3	917	2	Q75GM9_ORYSA	Q75gm9 oryza sativ	969	164.5	5.2	819	2	Q659A9_HUMAN	Q659a9 homo sapien	
897	167.5	5.3	1174	2	Q7XS37_ORYSA	Q7xs37 oryza sativ	970	164.5	5.2	858	1	LRRCS_HUMAN	Q711w4 homo sapien	
898	167	5.3	537	2	Q6P2A4_RAT	Q6p2a4 rattus norv	971	164	5.2	257	1	LRRCS_MOUSE	P59034 mus musculus	
899	167	5.3	582	2	Q6AY15_RAT	Q6ay15 rattus norv	972	164	5.2	257	2	Q543Z4_MOUSE	P59034 mus musculus	
900	167	5.3	633	2	Q8F3F6_LEPIN	Q8f3f6 leptospira	973	164	5.2	426	2	Q8F213_LEPIN	Q8f213 leptospira	
901	167	5.3	743	2	Q84CF7_LISMO	Q84cf7 listeria mo	974	164	5.2	515	2	Q60MT7_CABBR	Q60mt7 caenorhabdi	
902	167	5.3	744	2	Q8KTF4_LISMO	Q8kTf4 listeria mo	975	164	5.2	559	2	Q60UG7_CABBR	Q60ug7 caenorhabdi	
903	167	5.3	794	2	Q6YW99_ORYSA	Q6yw99 oryza sativ	976	164	5.2	570	2	Q8L3T8_ORYSA	Q8l3t8 oryza sativ	
904	167	5.3	838	1	TLR4_CRIGR	Q9wv82 cricetus	977	164	5.2	611	2	Q7TQ62_MOUSE	Q7tq62 mus musculus	
905	167	5.3	939	2	Q4SZU0_TETNG	Q4szu0 tetraodon n	978	164	5.2	696	1	SLIK1_HUMAN	Q7c6q2 homo sapien	
906	167	5.3	1112	2	Q41397_LYCPM	Q41397 lycopersico	979	164	5.2	696	1	SLIK1_MOUSE	Q810c1 mus musculus	
907	167	5.3	1112	2	Q41398_LYCPM	Q41398 lycopersico	980	164	5.2	696	2	Q5U516_HUMAN	Q5u516 homo sapien	

981	164	5.2	696	2	Q5RAC4_PONPY	Q5rac4	pongo pygma	1054	161	5.1	1019	2	Q4RW99_TETNG	Q4rw99	tetraodon n
982	164	5.2	760	2	Q63Z70_MOUSE	Q63z70	mus musculus	1055	160.5	5.1	487	2	Q7QKY2_ANOGA	Q7ky2	anopheles g
983	164	5.2	805	2	Q7QFF0_ANOGA	Q7qff0	anopheles g	1056	160.5	5.1	519	1	Q4GO2_MOUSE	Q4gzd9	mus musculus
984	164	5.2	828	1	LGR6_HUMAN	Q9hbx8	homo sapien	1057	160.5	5.1	519	1	Q4VBEG_MOUSE	Q4vbe9	mus musculus
985	164	5.2	833	2	Q7Q8I8_ANOGA	Q7q8i8	anopheles g	1058	160.5	5.1	1466	2	Q5EWY7_CTEID	Q5ewy7	ctenopharyn
986	164	5.2	839	2	Q8MIQ2_RABIT	Q8miq2	oryctolagus g	1059	160.5	5.1	664	2	Q9V8Z0_DROME	Q9v8z0	drosophila
987	164	5.2	870	2	Q6PCD4_HUMAN	Q6pcd4	homo sapien	1060	160.5	5.1	2910	2	Q55225_MOUSE	Q55225	mus musculus
988	164	5.2	904	1	TLR3_HUMAN	Q15455	homo sapien	1061	160.5	5.1	3889	2	Q6SSB8_CHLRE	Q6sse8	chlamydomon
989	164	5.2	904	2	Q504W0_HUMAN	Q504w0	homo sapien	1062	160	5.1	258	2	Q4GLJ6_EPTST	Q4glj6	epitretus
990	164	5.2	904	2	Q4VAL2_HUMAN	Q4val2	homo sapien	1063	160	5.1	518	2	Q4R5R9_MACFA	Q4r5r9	macaca fasc
991	164	5.2	1032	2	Q865B9_CANFA	Q865b9	canis famil	1064	160	5.1	744	2	Q65375_ARATH	Q65375	arabidopsis
992	164	5.2	1395	2	Q7SC01_NEUCR	Q7sc01	neurospora	1065	160	5.1	950	2	Q5H723_FUGRU	Q5h723	fugu rubrip
993	164	5.2	1913	2	Q5SVA2_HUMAN	Q5sva2	homo sapien	1066	160	5.1	1050	2	Q9BN18_DROME	Q9bn18	drosophila
994	164	5.2	2045	1	AGRN_HUMAN	Q00468	homo sapien	1067	160	5.1	1080	2	Q69P46_ORYSA	Q69p46	oryza sativ
995	164	5.2	2045	2	Q60FE1_HUMAN	Q60fe1	homo sapien	1068	160	5.1	1096	2	Q8W556_ARATH	Q8w556	arabidopsis
996	163.5	5.2	163	2	Q6E4H0_PETMA	Q6e4h0	petromyzon	1069	160	5.1	1402	1	LAP2_MOUSE	Q80th2	mus musculus
997	163.5	5.2	166	2	Q6E4H0_PETMA	Q6e4h0	petromyzon	1070	160	5.1	1496	2	Q92626_HUMAN	Q92626	homo sapien
998	163.5	5.2	180	2	Q6E4H7_PETMA	Q6e4h7	petromyzon	1071	159.5	5.1	187	2	Q6E415_PETMA	Q6e415	petromyzon
999	163.5	5.2	362	2	Q502F2_BRARE	Q502f2	brachydanio	1072	159.5	5.1	235	2	Q4G115_EPTST	Q4g115	epitretus
1000	163.5	5.2	370	2	Q9DE04_ORENI	Q9de04	oreochromis	1073	159.5	5.1	412	2	Q5MIQ1_AEDAL	Q5miq1	aedes albop
1001	163.5	5.2	582	2	Q5R5R1_PONPY	Q5r5r1	pongo pygma	1074	159.5	5.1	494	2	Q9LHF1_ARATH	Q9lhf1	arabidopsis
1002	163.5	5.2	671	2	Q53GZ4_HUMAN	Q53gz4	homo sapien	1075	159.5	5.1	520	1	AMG02_RAT	Q7tnj4	rattus norv
1003	163.5	5.2	786	2	Q48809_ARATH	Q48809	arabidopsis	1076	159.5	5.1	636	2	Q8SQH3_CANFA	Q8sqh3	canis famil
1004	163	5.2	359	2	Q9DE03_ORENI	Q9de03	oreochromis	1077	159.5	5.1	722	2	Q4KMG2_HUMAN	Q4kmg2	homo sapien
1005	163	5.2	452	2	Q4RQB6_TETNG	Q4rqb6	tetraodon n	1078	159.5	5.1	1112	2	Q64486_ARATH	Q64486	arabidopsis
1006	163	5.2	501	2	Q6ZHB5_ORYSA	Q6zhb5	oryza sativ	1079	159	5.1	257	1	LRR3_RAT	P59035	rattus norv
1007	163	5.2	524	2	Q8R378_MOUSE	Q8r378	mus musculus	1080	159	5.1	524	1	LRR3_HUMAN	Q9bct6	homo sapien
1008	163	5.2	582	1	SHOC2_MOUSE	Q88520	mus musculus	1081	159	5.1	524	2	Q5TGN3_HUMAN	Q5tgn3	homo sapien
1009	163	5.2	929	2	Q6P9N3_MOUSE	Q6p9n3	mus musculus	1082	159	5.1	543	2	Q8S7M7_ORYSA	Q8s7m7	oryza sativ
1010	163	5.2	933	2	Q9BJD5_STRPU	Q9bjd5	strongyloce	1083	159	5.1	550	1	LG12_MOUSE	Q8k4z0	mus musculus
1011	163	5.2	961	2	Q76CT7_PAROL	Q76ct7	paralichthy	1084	159	5.1	626	2	Q9NDB1_LEITR	Q9ndb1	leishmania
1012	163	5.2	961	2	Q76CT9_PAROL	Q76ct9	paralichthy	1085	159	5.1	671	2	Q60Y23_CABER	Q60y23	caenorhabdi
1013	163	5.2	1221	2	Q9BIW9_CABEL	Q9biw9	caenorhabdi	1086	159	5.1	695	2	Q93539_CABEL	Q93539	caenorhabdi
1014	163	5.2	1612	1	LAP4_MOUSE	Q80u72	mus musculus	1087	159	5.1	964	2	Q86U22_HUMAN	Q86u22	homo sapien
1015	162.5	5.2	283	2	Q9V4Z8_DROME	Q9v4z8	drosophila	1088	159	5.1	984	1	RIN3_HUMAN	Q86u22	homo sapien
1016	162.5	5.2	375	2	Q5XIH1_RAT	Q5xih1	rattus norv	1089	159	5.1	985	2	Q76Lb3_HUMAN	Q76lb3	homo sapien
1017	162.5	5.2	452	2	Q8FL18_LEPIN	Q8fl18	leptosira	1090	159	5.1	1119	2	Q8ZOH2_ANASP	Q8zoh2	anabaena sp
1018	162.5	5.2	494	2	Q9VEK6_DROME	Q9vek6	drosophila	1091	158.5	5.1	163	2	Q6E4E4_PETMA	Q6e4e4	petromyzon
1019	162.5	5.2	527	2	Q6FPB5_DROME	Q6fpb5	drosophila	1092	158.5	5.1	166	2	Q6E4B6_PETMA	Q6e4b6	petromyzon
1020	162.5	5.2	641	2	Q8MQM0_DROME	Q8mqm0	drosophila	1093	158.5	5.1	242	2	Q4SSH2_TETNG	Q4ssh2	tetraodon n
1021	162.5	5.2	700	2	Q4R6H5_MACFA	Q4r6h5	macaca fasc	1094	158.5	5.1	371	2	Q4T5R8_TETNG	Q4t5r8	tetraodon n
1022	162.5	5.2	1045	2	Q5H717_FUGRU	Q5h717	fugu rubrip	1095	158.5	5.1	417	2	Q15828_LEICH	Q15828	leishmania
1023	162	5.2	234	2	Q4G1H3_EPTST	Q4g1h3	epitretus	1096	158.5	5.1	656	2	Q19312_CABEL	Q19312	caenorhabdi
1024	162	5.2	242	2	Q9UG10_HUMAN	Q9ug10	homo sapien	1097	158.5	5.1	738	2	Q93373_CABEL	Q93373	caenorhabdi
1025	162	5.2	375	2	Q7Q1I8_ANOGA	Q7q1i8	anopheles g	1098	158.5	5.1	943	2	Q4S133_TETNG	Q4s133	tetraodon n
1026	162	5.2	613	2	Q7Z5L7_HUMAN	Q7z5l7	homo sapien	1099	158.5	5.1	953	2	Q9V701_DROME	Q9v701	drosophila
1027	162	5.2	642	2	Q6UXL8_HUMAN	Q6uxl8	homo sapien	1100	158.5	5.1	1007	2	Q8MQU9_AEDAE	Q8mqu9	aedes aegypt
1028	162	5.2	642	2	Q5VVZ2_HUMAN	Q5vvz2	homo sapien	1101	158.5	5.1	1032	1	TLR8_MOUSE	P58682	mus musculus
1029	162	5.2	649	2	Q8C2M4_MOUSE	Q8c2m4	mus musculus	1102	158.5	5.1	1061	2	Q655V6_ORYSA	Q655v6	oryza sativ
1030	162	5.2	661	2	Q6PIR3_HUMAN	Q6pir3	homo sapien	1103	158.5	5.1	1123	2	Q65XS7_ORYSA	Q65xs7	oryza sativ
1031	162	5.2	661	2	Q5VVZ3_HUMAN	Q5vvz3	homo sapien	1104	158.5	5.1	1181	2	Q7ZZ35_BRARE	Q7zz35	brachydanio
1032	161.5	5.2	942	2	Q7Q1S8_ANOGA	Q7q1s8	anopheles g	1105	158.5	5.1	1202	1	CSK12_HUMAN	Q8wx0	homo sapien
1033	162	5.2	1040	2	Q6Z8Y3_ORYSA	Q6z8y3	oryza sativ	1106	158.5	5.1	1300	2	Q9NKD6_DROME	Q9nkD6	drosophila
1034	161.5	5.2	259	2	Q7QHK8_ANOGA	Q7qhk8	anopheles g	1107	158	5.0	239	2	Q4KP19_9PETR	Q4kp19	ichthyomyzo
1035	161.5	5.2	268	2	Q4KP17_9PETR	Q4kp17	ichthyomyzo	1108	158	5.0	249	2	Q4KP07_LAMAP	Q4kp07	lampetra ap
1036	161.5	5.2	351	2	Q5KT50_XENLA	Q5kt50	xenopus lae	1109	158	5.0	317	2	Q6EB32_HUMAN	Q6eb32	homo sapien
1037	161.5	5.2	507	2	Q9N3F2_CABEL	Q9n3f2	caenorhabdi	1110	158	5.0	352	1	KERA_HUMAN	Q60938	homo sapien
1038	161.5	5.2	519	2	Q7Q1I6_ANOGA	Q7q1i6	anopheles g	1111	158	5.0	377	2	Q72U33_LEPIC	Q72u33	leptosira
1039	161.5	5.2	841	1	TLR4_BOVIN	Q9gl65	bos taurus	1112	158	5.0	510	2	Q9N1R8_DICDI	Q9n1r8	dictyosteli
1040	161.5	5.2	841	2	Q6WCD4_BOVIN	Q6wcd4	bos taurus	1113	158	5.0	531	2	Q5TW51_ANOGA	Q5tw51	anopheles g
1041	161.5	5.2	841	2	Q6WCD5_BOVIN	Q6wcd5	bos taurus	1114	158	5.0	677	2	Q5XPV7_ICTPU	Q5xpv7	ictalurys p
1042	161.5	5.2	841	2	Q8SQ55_BOVIN	Q8sq55	bos taurus	1115	158	5.0	741	2	Q9VJA9_DROME	Q9vja9	drosophila
1043	161.5	5.2	1193	2	Q4SL20_TETNG	Q4sl20	tetraodon n	1116	158	5.0	838	2	Q4SWS3_TETNG	Q4sws3	tetraodon n
1044	161.5	5.2	1270	2	Q5RK15_RAT	Q5rk15	rattus norv	1117	158	5.0	879	2	Q68C13_ONCMY	Q68c13	oncorhynch
1045	161	5.1	397	2	Q7QF88_ANOGA	Q7qf88	anopheles g	1118	158	5.0	909	2	Q6ZRC2_HUMAN	Q6zrc2	homo sapien
1046	161	5.1	558	2	Q8MPP6_CABEL	Q8mpp6	caenorhabdi	1119	158	5.0	1032	2	Q56R09_AOTNA	Q56r09	actus nancy
1047	161	5.1	559	2	Q22875_CABEL	Q22875	caenorhabdi	1120	158	5.0	5703	1	MUC5B_HUMAN	Q9hc84	homo sapien
1048	161	5.1	586	2	Q93377_CABEL	Q93377	caenorhabdi	1121	157.5	5.0	163	2	Q6E414_PETMA	Q6e414	petromyzon
1049	161	5.1	682	1	CONN_DROME	Q01819	drosophila	1122	157.5	5.0	224	2	Q9DE01_BRARE	Q9de01	brachydanio
1050	161	5.1	691	2	Q6AWM0_DROME	Q6awm0	drosophila	1123	157.5	5.0	272	2	Q7KWF0_DROME	Q7kwf0	drosophila
1051	161	5.1	861	2	Q9SLS3_TOBAC	Q9sls3	nicotiana t	1124	157.5	5.0	276	2	Q7PSP4_ANOGA	Q7psp4	anopheles g
1052	161	5.1	905	2	Q7TN18_RAT	Q7tni8	rattus norv	1125	157.5	5.0	396	2	Q5DZ80_VIBF1	Q5dz80	vibrio fisc
1053	161	5.1	945	2	Q801F9_CARAU	Q801f9	carassius a	1126	157.5	5.0	655	2	Q4RW74_TETNG	Q4rw74	tetraodon n

1127	157.5	5.0	861	2	Q50TQ5_ENTHI	Q50tcq5 entamoeba h	1200	154.5	4.9	2461	2	Q56D06_HUMAN	Q56d06 homo sapien
1128	157.5	5.0	1102	2	Q4R2Y0_TETNG	Q4ry20 tetraodon n	1201	154.5	4.9	2517	1	NCOR2_HUMAN	Q9y618 h nuclear r
1129	157.5	5.0	2657	2	Q4S189_TETNG	Q4s189 tetraodon n	1202	154	4.9	399	2	Q8STX6_ENCCU	Q8stx6 encephalic
1130	157	5.0	266	2	Q7Q1P7_ANOGA	Q7qlp7 anopheles g	1203	154	4.9	458	2	Q9VU13_DROME	Q9vul3 drosophila
1131	157	5.0	273	2	Q9NUU4_HUMAN	Q9nuu4 homo sapien	1204	154	4.9	491	2	Q6KAP0_MOUSE	Q6kap0 mus musculu
1132	157	5.0	377	2	Q8F119_LEPIN	Q8f119 leptospira	1205	154	4.9	530	2	P97830_RAT	P97830 rattus norv
1133	157	5.0	444	2	Q9HSH8_HUMAN	Q9hsh8 homo sapien	1206	154	4.9	584	2	Q49751_ARATH	Q49751 arabidopsis
1134	157	5.0	592	2	Q7L236_HUMAN	Q7l236 homo sapien	1207	154	4.9	584	2	Q8L722_ARATH	Q8l722 arabidopsis
1135	157	5.0	613	2	Q940E8_MAIZE	Q940e8 zea mays [m	1208	154	4.9	812	2	Q9VFY9_DROME	Q9vfy9 drosophila
1136	157	5.0	622	2	Q8N3B0_HUMAN	Q8n3b0 homo sapien	1209	154	4.9	825	2	Q63U08_BURPS	Q63u08 burkholderi
1137	157	5.0	680	1	LRCH4_MOUSE	Q921g6 mus musculu	1210	154	4.9	953	2	Q8VYG7_ARATH	Q8vyg7 arabidopsis
1138	157	5.0	796	2	Q6NSJ5_HUMAN	Q6nsj5 homo sapien	1211	154	4.9	965	2	Q8H724_FUGRU	Q8h724 fugu rubrip
1139	157	5.0	903	2	Q6LW15_BRARE	Q6lw15 brachydanio	1212	154	4.9	1845	2	Q80U08_MOUSE	Q80u08 mus musculu
1140	157	5.0	1032	2	Q6Y12M6_RAT	Q6y12m6 rattus norv	1213	153.5	4.9	163	2	Q6E4L8_PETMA	Q6e4l8 petromyzon
1141	157	5.0	1032	2	Q6Y1S0_RAT	Q6y1s0 rattus norv	1214	153.5	4.9	166	2	Q6E4G9_PETMA	Q6e4g9 petromyzon
1142	156.5	5.0	305	2	Q50Q05_ENTHI	Q50q05 entamoeba h	1215	153.5	4.9	246	2	Q4KP02_LAMAP	Q4kp02 lampetra ap
1143	156.5	5.0	360	1	PGS2_RABIT	Q28888 oryctolagus	1216	153.5	4.9	366	2	Q5R858_PONPY	Q5r858 pongo pygma
1144	156.5	5.0	376	1	FMOD_HUMAN	Q06828 homo sapien	1217	153.5	4.9	389	2	Q4RHN3_TETNG	Q4rhn3 tetraodon n
1145	156.5	5.0	428	2	Q9VDD4_DROME	Q9vdd4 drosophila	1218	153.5	4.9	403	2	Q96CX6_HUMAN	Q96cx6 homo sapien
1146	156.5	5.0	487	2	Q7Q087_ANOGA	Q7q087 anopheles g	1219	153.5	4.9	526	2	Q5BL36_BRARE	Q5bl36 brachydanio
1147	156.5	5.0	505	2	Q4RVS9_TETNG	Q4rvs9 tetraodon n	1220	153.5	4.9	655	2	Q9FBR7_STRCO	Q9fbr7 streptomyce
1148	156.5	5.0	524	2	Q6AXP5_RAT	Q6axp5 rattus norv	1221	153.5	4.9	685	2	Q72TH0_LBPIC	Q72th0 leptospira
1149	156.5	5.0	551	2	Q5ZB68_ORYSA	Q5zb68 oryza sativ	1222	153.5	4.9	805	2	Q8F1V0_LBPIN	Q8f1v0 leptospira
1150	156.5	5.0	711	2	Q9SPM1_LYCES	Q9spm1 lycopersico	1223	153.5	4.9	802	2	Q8L4U4_ORYSA	Q8l4u4 oryza sativ
1151	156.5	5.0	887	1	UFO_HUMAN	P30330 homo sapien	1224	153.5	4.9	864	2	Q8LPG4_ARATH	Q8lp94 arabidopsis
1152	156.5	5.0	980	2	Q92U10_ARATH	Q92u10 arabidopsis	1225	153.5	4.9	864	2	Q9T033_ARATH	Q9t033 arabidopsis
1153	156.5	5.0	1179	2	Q7PMD3_ANOGA	Q7pmd3 anopheles g	1226	153.5	4.9	894	2	Q8N5L2_HUMAN	Q8n5l2 homo sapien
1154	156.5	5.0	1301	2	Q9VZ81_DROME	Q9vz81 drosophila	1227	153.5	4.9	940	2	Q4RGH3_TETNG	Q4rgh3 tetraodon n
1155	156.5	5.0	1766	2	Q6XHA8_DICDI	Q6xha8 dictyosteli	1228	153.5	4.9	987	2	Q53MD2_ORYSA	Q53md2 oryza sativ
1156	156.5	5.0	1867	2	Q54M77_DICDI	Q54m77 dictyosteli	1229	153.5	4.9	1032	1	TLR9_HUMAN	Q9nr96 homo sapien
1157	156	5.0	163	2	Q6S4D2_PETMA	Q6s4d2 petromyzon	1230	153.5	4.9	1041	2	Q9FI15_ARATH	Q9fi15 arabidopsis
1158	156	5.0	163	2	Q6S4F5_PETMA	Q6s4f5 petromyzon	1231	153.5	4.9	1110	2	Q9FI77_ARATH	Q9fi77 arabidopsis
1159	156	5.0	257	1	LRRC3_HUMAN	Q9by71 homo sapien	1232	153.5	4.9	1121	2	Q942F3_ORYSA	Q942f3 oryza sativ
1160	156	5.0	354	1	PGS2_RAT	Q01129 rattus norv	1233	153.5	4.9	1388	2	Q4RIV6_TETNG	Q4riv6 tetraodon n
1161	156	5.0	422	2	Q4RH13_TETNG	Q4rh13 tetraodon n	1234	153.5	4.9	3247	2	Q6S553_9ALPH	Q6s553 bovine herp
1162	156	5.0	469	2	Q9WL28_DROME	Q9wl28 drosophila	1235	153.5	4.9	3247	2	Q77CD4_9ALPH	Q77cd4 bovine herp
1163	156	5.0	547	2	Q4QI16_LEIMA	Q4q116 leishmania	1236	153	4.9	367	2	Q6GLE8_XENTR	Q6gle8 xenopus tro
1164	156	5.0	552	2	Q8K375_MOUSE	Q8k375 mus musculu	1237	153	4.9	529	2	Q4F4C4_CHICK	Q4f4c4 gallus gall
1165	156	5.0	575	2	Q571F2_MOUSE	Q571f2 mus musculu	1238	153	4.9	548	2	Q4V8C9_RAT	Q4v8c9 rattus norv
1166	156	5.0	594	2	Q9U3A0_CAEEL	Q9u3a0 caenorhabdi	1239	153	4.9	581	2	Q9D5Q5_MOUSE	Q9d5q5 m mus muscu
1167	156	5.0	643	2	Q6QI48_RAT	Q6qi48 rattus norv	1240	153	4.9	590	2	Q9D2F4_MOUSE	Q9d2f4 m mus muscu
1168	156	5.0	704	2	Q4QK11_LEIMA	Q4qk11 leishmania	1241	153	4.9	699	1	VGLG_HV2H	V13290 human herpe
1169	156	5.0	940	2	Q8T753_BRAFL	Q8t753 brachyosteo	1242	153	4.9	720	2	Q6PQA5_HPAU	Q6pqa5 sparus aua
1170	156	5.0	953	2	Q617Q9_CABER	Q617q9 caenorhabdi	1243	153	4.9	1840	2	Q9ULI4_HUMAN	Q9uli4 homo sapien
1171	156	5.0	1039	2	Q8GBL1_DROME	Q8gbl1 drosophila	1244	153	4.9	2042	1	MDC1_PIG	Q76718 sus scrofa
1172	155.5	5.0	332	2	Q6C2U8_YARLI	Q6c2u8 yarrowia li	1245	152.5	4.9	163	2	Q5E4F3_PETMA	Q5e4f3 petromyzon
1173	155.5	5.0	338	2	Q6VEX8_CHICK	Q6vex8 gallus gall	1246	152.5	4.9	370	2	Q5R9V7_PONPY	Q5r9v7 pongo pygma
1174	155.5	5.0	367	2	Q8BK43_MOUSE	Q8bk43 mus musculu	1247	152.5	4.9	372	2	Q5VZS8_HUMAN	Q5vzs8 homo sapien
1175	155.5	5.0	664	2	Q5EWY6_CTEID	Q5ewy6 ctenopharyn	1248	152.5	4.9	550	2	Q7PT66_ANOGA	Q7pt66 anopheles g
1176	155.5	5.0	980	2	Q8QWA0_MOUSE	Q8qwa0 mus musculu	1249	152.5	4.9	577	2	Q8AVI4_XENLA	Q8avi4 xenopus lae
1177	155.5	5.0	1102	2	Q8KC98_CHLTE	Q8kc98 chlorobium	1250	152.5	4.9	581	2	Q9AN90_BRAJA	Q9an90 bradyrhizob
1178	155.5	5.0	1135	2	Q8ARP6_ARATH	Q8arp6 arabidopsis	1251	152.5	4.9	585	2	Q89TL5_BRAJA	Q89tl5 bradyrhizob
1179	155.5	5.0	1285	1	CRUM2_HUMAN	Q5ij48 homo sapien	1252	152.5	4.9	849	1	LAP1_DROME	Q9v780 drosophila
1180	155.5	5.0	1334	2	Q9RRK9_STRCO	Q9rrk9 streptomyce	1253	152.5	4.9	1047	2	Q5H719_FUGRU	Q5h719 fugu rubrip
1181	155	4.9	347	2	Q9DE00_PETMA	Q9de00 petromyzon	1254	152.5	4.9	1109	2	Q8H4J0_ORYSA	Q8h4j0 oryza sativ
1182	155	4.9	504	1	AMGQ3_HUMAN	Q866wk7 homo sapien	1255	152.5	4.9	1287	2	Q5TMV4_AMOGA	Q5tmv4 anopheles g
1183	155	4.9	576	2	Q6ZBP4_ORYSA	Q6zbp4 oryza sativ	1256	152.5	4.9	1295	2	Q8T0X1_BOMMO	Q8t0x1 bombyx mori
1184	155	4.9	719	2	Q8VJQ6_MYCTU	Q8vjq6 mycobacteri	1257	152.5	4.9	1356	2	Q8WRE2_ANOGA	Q8wre2 anopheles g
1185	155	4.9	825	2	Q6ZJU6_BURNA	Q6zju6 burkholderi	1258	152.5	4.9	1817	2	Q4WMC5_ASFFU	Q4wmc5 aspergillus
1186	155	4.9	961	2	P90920_CAEEL	P90920 caenorhabdi	1259	152.5	4.9	3288	2	Q7T5D9_CHV1	Q7t5d9 cercopithe
1187	155	4.9	1041	1	TLR8_HUMAN	Q9nr97 homo sapien	1260	152	4.8	443	1	LRC17_MOUSE	Q9cxd9 mus musculu
1188	154.5	4.9	219	2	Q90WZ2_CHICK	Q90wz2 gallus gall	1261	152	4.8	562	2	Q9M7W9_ARATH	Q9m7w9 arabidopsis
1189	154.5	4.9	246	2	Q4KP18_9PETR	Q4kp18 ichtthyomz	1262	152	4.8	682	2	Q5JN60_ORYSA	Q5jn60 oryza sativ
1190	154.5	4.9	376	2	Q8IV47_HUMAN	Q8iv47 homo sapien	1263	152	4.8	776	2	Q6R2K3_ARATH	Q6r2k3 arabidopsis
1191	154.5	4.9	524	1	LRRC1_MOUSE	Q80vq1 mus musculu	1264	152	4.8	786	1	TLR1_HUMAN	Q15399 homo sapien
1192	154.5	4.9	548	2	Q9VJUI_DROME	Q9vjui drosophila	1265	152	4.8	786	2	Q6FI64_HUMAN	Q6fi64 homo sapien
1193	154.5	4.9	606	2	Q57IM3_MOUSE	Q57im3 mus musculu	1266	152	4.8	786	2	Q5FWG5_HUMAN	Q5fwg5 homo sapien
1194	154.5	4.9	631	2	Q8TN14_METAC	Q8tn14 methanocarc	1267	152	4.8	796	1	TLR6_HUMAN	Q9v2c9 homo sapien
1195	154.5	4.9	1013	2	Q9M0G7_ARATH	Q9m0g7 arabidopsis	1268	152	4.8	863	2	Q4R6F0_MACFA	Q4r6f0 macaca fasc
1196	154.5	4.9	1109	2	Q6YT77_ORYSA	Q6yt77 oryza sativ	1269	151.5	4.8	347	2	Q9D9Q0_MOUSE	Q9d9q0 mus musculu
1197	154.5	4.9	1143	2	Q9SUB9_ARATH	Q9sub9 arabidopsis	1270	151.5	4.8	507	2	Q6IX12_CABBR	Q6ix12 caenorhabdi
1198	154.5	4.9	1192	1	EXS_ARATH	Q9lyn8 arabidopsis	1271	151.5	4.8	623	2	Q7Q090_ANOGA	Q7q090 anopheles g
1199	154.5	4.9	1961	2	Q6MG89_RAT	Q6mg89 rattus norv	1272	151.5	4.8	710	2	Q5TR39_ANOGA	Q5tr39 anopheles g

1273	151.5	4.8	855	2	08L3Y5_SOYBN	Q8L3Y5 glycine max
1274	151.5	4.8	997	2	06K7X5_ORYSA	Q6K7X5 oryza sativ
1275	151.5	4.8	998	2	04W9M1_ASFPU	Q4W9M1 aspergillus
1276	151.5	4.8	1109	2	Q84ZJ8_ORYSA	Q84ZJ8 oryza sativ
1277	151.5	4.8	1152	2	Q7PFC4_ANOGA	Q7PFC4 anopheles g
1278	151.5	4.8	1152	2	Q8WRE5_ANOGA	Q8WRE5 anopheles g
1279	151.5	4.8	1775	2	054811_DICDI	Q54811 dictyosteli
1280	151	4.8	163	2	0654H9_PETMA	Q654H9 petromyzon
1281	151	4.8	399	2	Q8BM45_MOUSE	Q8BM45 m mus muscu
1282	151	4.8	508	2	050Z76_ENTHI	Q50Z76 entamoeba h
1283	151	4.8	530	2	Q08934_MOUSE	Q08934 mus musculu
1284	151	4.8	540	2	Q6V6S6_DROSI	Q6V6S6 drosophila
1285	151	4.8	540	2	P93666_HELAN	P93666 helianthus
1286	151	4.8	541	2	Q6V6S8_DROSI	Q6V6S8 drosophila
1287	151	4.8	541	2	Q6V6S8_DROSI	Q6V6S8 drosophila
1288	151	4.8	541	2	Q6V6T0_DROSI	Q6V6T0 drosophila
1289	151	4.8	581	2	Q04143_SILLA	Q04143 silene lati
1290	151	4.8	784	2	Q6YGU2_RAT	Q6YGU2 rattus norv
1291	151	4.8	793	2	Q704V6_BOVIN	Q704V6 bos taurus
1292	151	4.8	793	2	Q706D2_BOVIN	Q706D2 bos taurus
1293	151	4.8	835	1	TLR4_MOUSE	TLR4 mouse
1294	151	4.8	835	2	Q5RG74_MOUSE	Q5RG74 mus musculu
1295	151	4.8	947	2	Q8RUT5_ORYSA	Q8RUT5 oryza sativ
1296	151	4.8	1030	2	Q8H037_ORYSA	Q8H037 oryza sativ
1297	151	4.8	1385	2	Q9V8Z5_DROME	Q9V8Z5 drosophila
1298	151	4.8	1389	2	Q24591_DROME	Q24591 drosophila
1299	150.5	4.8	289	2	Q8F3F4_LEPIN	Q8F3F4 leptospira
1300	150.5	4.8	329	2	Q8F115_LEPIN	Q8F115 leptospira
1301	150.5	4.8	408	2	Q8F212_LEPIN	Q8F212 leptospira
1302	150.5	4.8	413	2	Q72TC4_LEPIC	Q72TC4 leptospira
1303	150.5	4.8	423	1	OMD_RAT	OMD rat
1304	150.5	4.8	537	2	Q9C769_ARATH	Q9C769 arabidopsis
1305	150.5	4.8	641	2	Q4TBJ8_TETNG	Q4TBJ8 tetraodon n
1306	150.5	4.8	648	2	Q8BU93_MOUSE	Q8BU93 m mus muscu
1307	150.5	4.8	685	2	Q6AXL3_BRARE	Q6AXL3 brachydanio
1308	150.5	4.8	695	1	FSHR_HUMAN	FSHR human
1309	150.5	4.8	695	1	Q4ORJ3_HUMAN	Q4ORJ3 homo sapien
1310	150.5	4.8	818	2	Q75CU0_PAROL	Q75CU0 paralicthy
1311	150.5	4.8	871	2	Q5H726_FUGRU	Q5H726 fugu rubrip
1312	150.5	4.8	1107	2	Q8BKp3_MOUSE	Q8BKp3 m mus muscu
1313	150.5	4.8	1109	1	RPX1_IPONI	RPX1 ipomoea nil
1314	150.5	4.8	1140	2	Q9LR04_ARATH	Q9LR04 arabidopsis
1315	150.5	4.8	1149	2	Q6GOR9_MOUSE	Q6GOR9 mus musculu
1316	150.5	4.8	1461	2	Q94H87_ORYSA	Q94H87 oryza sativ
1317	150.5	4.8	1702	2	Q7FS33_ANOGA	Q7FS33 anopheles g
1318	150.5	4.8	1898	2	Q6ZP14_MOUSE	Q6ZP14 mus musculu
1319	150.5	4.8	1944	2	Q4S1G7_TETNG	Q4S1G7 tetraodon n
1320	150	4.8	163	2	Q654E8_PETMA	Q654E8 macaca fasc
1321	150	4.8	239	2	Q4KP08_LAMAP	Q4KP08 lampetra ap
1322	150	4.8	259	1	LRC3B_HUMAN	LRC3B homo sapien
1323	150	4.8	259	1	LRC3B_MOUSE	LRC3B mus musculu
1324	150	4.8	259	2	Q5M8T0_HUMAN	Q5M8T0 homo sapien
1325	150	4.8	259	2	Q543Z7_MOUSE	Q543Z7 mus musculu
1326	150	4.8	272	1	PGS1_PIG	PGS1 sus scrofa
1327	150	4.8	305	2	Q9N0Z8_MACFA	Q9N0Z8 macaca fasc
1328	150	4.8	342	2	Q4V9E0_BRARE	Q4V9E0 brachydanio
1329	150	4.8	348	2	Q756S8_ASHGO	Q756S8 ashbya goss
1330	150	4.8	367	2	Q86X40_HUMAN	Q86X40 homo sapien
1331	150	4.8	584	2	Q49750_ARATH	Q49750 arabidopsis
1332	150	4.8	594	2	Q4SDI8_TETNG	Q4SDI8 tetraodon n
1333	150	4.8	652	2	Q8GUM9_ARATH	Q8GUM9 arabidopsis
1334	150	4.8	796	2	Q5SHIC_PIG	Q5SHIC sus scrofa
1335	150	4.8	796	2	Q76L23_PIG	Q76L23 pig
1336	150	4.8	802	2	Q8LFN2_ARATH	Q8LFN2 arabidopsis
1337	150	4.8	803	2	Q9SRV4_ARATH	Q9SRV4 arabidopsis
1338	150	4.8	1294	2	Q8ZV77_ORYSA	Q8ZV77 oryza sativ
1339	150	4.8	1305	1	TCGAP_MOUSE	TCGAP mus musculu
1340	150	4.8	1315	1	CHAO_DROME	CHAO drosophila
1341	149.5	4.8	98	2	Q9XG3_CHICK	Q9XG3 gallus gall
1342	149.5	4.8	163	2	Q654E9_PETMA	Q654E9 petromyzon
1343	149.5	4.8	164	2	Q654E8_PETMA	Q654E8 petromyzon
1344	149.5	4.8	167	2	Q6E4I1_PETMA	Q6E4I1 petromyzon
1345	149.5	4.8	224	2	Q44086_CABEL	Q44086 caenorhabdi

Q6V4C6_DROVA	2	542	4.8	149.5	1346	Q8L3Y5 glycine max
Q6L569_ORYSA	2	657	4.8	149.5	1347	Q6K7X5 oryza sativ
Q8G9F8_cynops pyrr	2	696	4.8	149.5	1348	Q4W9M1 aspergillus
Q8YR12 arabidopsis	2	894	4.8	149.5	1349	Q84ZJ8 oryza sativ
Q8XFM6 oryza sativ	2	957	4.8	149.5	1350	Q7PFC4 ANOGA
Q8S7A6 oryza sativ	2	1056	4.8	149.5	1351	Q8WRE5 ANOGA
Q51A9 entamoeba h	2	1056	4.8	149.5	1352	Q54811 dictyosteli
Q51A9 entamoeba h	2	1469	4.8	149.5	1353	Q654H9 petromyzon
Q64AD3 petromyzon	2	1791	4.8	149.5	1354	Q8BM45 mouse
Q6E4D3 petromyzon	2	195	4.8	149	1355	Q50Z76 entamoeba h
Q86DD0 caenorhabdi	2	265	4.8	149	1356	Q08934 mouse
Q86S81 caenorhabdi	2	310	4.8	149	1357	Q6V6S6 drosophila
Q9NSD7 caenorhabdi	2	341	4.8	149	1358	P93666 helianthus
Q9HQ2 anopheles g	2	366	4.8	149	1359	Q6V6S8 drosophila
Q9N425 caenorhabdi	2	375	4.8	149	1360	Q6V6S8 drosophila
Q7PNQ0 anopheles g	2	421	4.8	149	1361	Q6V6T0 drosophila
Q7G6S9 anopheles g	2	437	4.8	149	1362	Q04143 silene lati
Q9LRV8 arabidopsis	2	471	4.8	149	1363	Q6YGU2 rattus norv
Q4G5Q5 leishmania	2	763	4.8	149	1364	Q704V6 bos taurus
Q91F8 cricetus	2	784	4.8	149	1365	Q706D2 bos taurus
Q8N537 homo sapien	2	927	4.8	149	1366	Q9QUK6 mus musculu
Q5AXH5 aspergillus	2	972	4.8	149	1367	Q5RG74 mouse
Q40640 oryza sativ	2	1025	4.8	149	1368	Q8RUT5 oryza sativ
Q7DMC2 oryza longi	2	1025	4.8	149	1369	Q8H037 oryza sativ
Q9ZP59 arabidopsis	2	1143	4.8	149	1370	Q9V8Z5 drosophila
Q53JZ9 oryza sativ	2	1164	4.8	149	1371	Q24591 drosophila
Q9UES6 homo sapien	2	1504	4.8	149	1372	Q8F3F4 leptospira
Q6P1B4 homo sapien	2	1504	4.8	149	1373	Q8F115 leptospira
Q7Z2X6 homo sapien	2	1504	4.8	149	1374	Q8F212 leptospira
Q6PGP3 homo sapien	2	1504	4.8	149	1375	Q72TC4 leptospira
Q15069 homo sapien	2	1522	4.8	149	1376	Q92187 rattus norv
Q9Y211 homo sapien	2	1528	4.8	149	1377	Q9C769 arabidopsis
Q75F93 ashbya goss	2	1874	4.8	149	1378	Q4TBJ8 tetraodon n
Q869S1 dictyosteli	2	2357	4.8	149	1379	Q8BU93 m mus muscu
Q9U1M8 dictyosteli	2	2357	4.8	149	1380	Q6AXL3 brachydanio
Q6E4F7 petromyzon	2	163	4.7	148.5	1381	P23945 homo sapien
Q91VH8 mus musculu	2	215	4.7	148.5	1382	Q4QRJ3 human
Q5C508 homo sapien	2	232	4.7	148.5	1383	Q75CU0 paralicthy
Q6X8P9 bos taurus	2	321	4.7	148.5	1384	Q5H726 fugu rubrip
P13605 bos taurus	2	375	4.7	148.5	1385	Q8BKp3 m mus muscu
P50609 rattus norv	2	376	4.7	148.5	1386	P93194 ipomoea nil
Q4T9I8 tetraodon n	2	516	4.7	148.5	1387	Q9LR04 arabidopsis
Q21604 caenorhabdi	2	610	4.7	148.5	1388	Q6GQR9 mus musculu
Q8PQD3 xanthomonas	2	646	4.7	148.5	1389	Q94H87 oryza sativ
Q93374 caenorhabdi	2	680	4.7	148.5	1390	Q7P639 anopheles g
P32212 macaca fasc	2	687	4.7	148.5	1391	Q6ZP14 mus musculu
Q6PG2 caenorhabdi	2	695	4.7	148.5	1392	Q4S1G7 tetraodon n
Q6GPJ8 xenopus lae	2	807	4.7	148.5	1393	Q6E4E8 petma
Q91Q11 arabidopsis	2	890	4.7	148.5	1394	Q4KP08 lampetra ap
Q8YV77 arabidopsis	2	964	4.7	148.5	1395	Q5PB08 homo sapien
Q9LY03 arabidopsis	2	964	4.7	148.5	1396	Q8VCH9 mus musculu
Q96PY9 homo sapien	2	1013	4.7	148.5	1397	Q5M8T0 homo sapien
Q91RT1 arabidopsis	2	1016	4.7	148.5	1398	Q543Z7 mus musculu
Q8WXE4 homo sapien	2	1099	4.7	148.5	1399	Q9GKQ6 sus scrofa
P46023 lymnaea ata	2	1115	4.7	148.5	1400	Q9N0Z8 macaca fasc
Q7S718 neurospora	2	1140	4.7	148.5	1401	Q4V9E0 brachydanio
Q4TJ85 tetraodon n	2	1279	4.7	148.5	1402	Q756S8 ashbya goss
Q8F116 leptospira	2	311	4.7	148	1403	Q86X40 homo sapien
P51886 rattus norv	2	338	4.7	148	1404	Q49750 arabidopsis
Q7S279 leptospira	2	449	4.7	148	1405	Q4SDI8 tetraodon n
Q505F5 mus musculu	2	572	4.7	148	1406	Q8GUM9 arabidopsis
Q4REF6 tetng	2	581	4.7	148	1407	Q5SHIC sus scrofa
Q651V0 oryza sativ	2	724	4.7	148	1408	Q76L23 pig
Q89X06 BRAJA	2	745	4.7	148	1409	Q8LFN2 arabidopsis
Q59H15 pig	2	811	4.7	148	1410	Q9SRV4 arabidopsis
Q41DR6 pig	2	811	4.7	148	1411	Q8ZV77 oryza sativ
Q5SMW5_ORYSA	2	915	4.7	148	1412	Q80YF9 mus musculu
Q6URA2_9ROSA	2	1095	4.7	148	1413	P12024 drosophila
Q41805_WAIZE	2	1188	4.7	148	1414	Q90XG3 gallus gall
1 NOTC4_MOUSE	1	1964	4.7	148	1415	Q6E4E8 petromyzon
Q75T35_GLOLA	2	2143	4.7	148	1416	Q6498 petromyzon
Q6E4M8_PETMA	2	163	4.7	147.5	1417	Q6E4I1 petromyzon
					1418	Q44086 caenorhabdi



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QY 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFQCPATTTTATVTPTRPVPREPTALSSSL 300  
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Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPGEG 360  
QY 361 FTGLYCESOMGOTRPSPTPTPRPSRLTLGIEPVSPSLRVGLQRYLQSSVOLRLSLR 420  
Db 361 FTGLYCESOMGOTRPSPTPTPRPSRLTLGIEPVSPSLRVGLQRYLQSSVOLRLSLR 420  
QY 421 LTYRNLSGDKRLVTLRLPASLAETVTQLRPNATYSVCVMPFGPRVPEGEACGEAHT 480  
Db 421 LTYRNLSGDKRLVTLRLPASLAETVTQLRPNATYSVCVMPFGPRVPEGEACGEAHT 480  
QY 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLAALAAVGAAYCVRGRAMAAAAQKGV 540  
Db 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLAALAAVGAAYCVRGRAMAAAAQKGV 540  
QY 541 GPGAGPLELEGVKVPLEPGPKATGEGGALPGSGCEVPLMGFPGQLGSLPHAKPYI 598  
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ID Q6UXL4 HUMAN PRELIMINARY; PRT; 673 AA.  
AC Q6UXL4;  
DT 05-JUL-2004 (TremBLrel. 27, Created)  
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)  
DE CSRV314 (Slit-like 2).  
GN Name=SLIT2; ORFName=UNQ314;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vanden R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,  
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Placenta;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzly D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RG NIH MGC Project;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY358299; AAQ88666.1; -; mRNA.  
DR EMBL; BC068575; AAH68575.1; -; mRNA.  
DR Ensembl; ENSG00000168140; Homo sapiens.  
DR InterPro; IPR000742; EGF 2.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR Cterm.  
DR InterPro; IPR003885; LRR cyst.  
DR InterPro; IPR00372; LRR Nterm.  
DR InterPro; IPR003591; LRR typ.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00041; fn3; 1.  
DR Pfam; PF00560; LRR 1; 6.  
DR Pfam; PF01462; LRRNT; 1.  
DR PRINTS; PR00019; LEURICHRPT.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00365; LRR SD22; 4.  
DR SMART; SM00369; LRR typ; 8.  
DR SMART; SM00082; LRRCT; 1.  
DR SMART; SM00013; LRRNT; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00026; EGF\_3; 1.  
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SQ SEQUENCE 673 AA; 71655 MW; 4CDAFA391231D4BF8 CRC64;  
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Matches 597; Conservative 1;  
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Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPGEG 360  
QY 361 FTGLYCESOMGOTRPSPTPTPRPSRLTLGIEPVSPSLRVGLQRYLQSSVOLRLSLR 420  
Db 361 FTGLYCESOMGOTRPSPTPTPRPSRLTLGIEPVSPSLRVGLQRYLQSSVOLRLSLR 420  
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QY 541 GPGAGPLELEGVKVPLEPGPKATGEGGALPGSGCEVPLMGFPGQLGSLPHAKPYI 598  
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RESULT 2  
ID Q6UXL4 HUMAN PRELIMINARY; PRT; 673 AA.  
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DT 05-JUL-2004 (TremBLrel. 27, Created)  
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)  
DE CSRV314 (Slit-like 2).  
GN Name=SLIT2; ORFName=UNQ314;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vanden R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,  
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

Db 181 LLALEPGILDANVEALRLAGLGLQQLDEGLFRLRLNHLHDLDVSDNQLERVPVIRGLRG 240  
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Db 241 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLIAAARNPF 300  
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Db 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 360  
QY 286 TRPVREPTALSSSLAPTWSPTAPATEAPSPESTAPPTVGPVPOQDCPPSTCLNGGTC 345  
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QY 346 HLGTRHHLACLCEGFTGLYCESQMGQGTFRPSTPTVTPRPSRLTLGIEPVSTSLRVGL 405  
Db 421 HLGTRHHLACLCEGFTGLYCESQMGQGTFRPSTPTVTPRPSRLTLGIEPVSTSLRVGL 480  
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Db 541 GRVPEGEACGEAHTPPAVHSHAPVTOAREGNLPLIIAPALAAVLLAALAAVGAAYCVR 600  
QY 526 RGRAMAAAQDKGVQFGAGPLEGKVPKATGEGGALPSGSECEVPLMGFP 585  
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QY 586 PGLQSPHAKPYI 598  
Db 661 PGLQSPHAKPYI 673

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AC Q6EMK4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
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GN Name=SLITL2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
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RX PubMed=15247411; DOI=10.1073/pnas.0404117101;  
RA Ikeda Y., Imai Y., Kumagai H., Nosaoka T., Morikawa Y., Hiseoka T.,  
RA Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,  
RA Nagai R., Kitamura T.;  
RT "Vasorin, a transforming growth factor [beta]-binding protein  
RT expressed in vascular smooth muscle cells, modulates the arterial  
RT response to injury in vivo.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).  
DR EMBL; AY166584; AAO27704.1; -; mRNA.  
DR Ensembl; ENSG00000168140; Homo sapiens.  
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DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR Cterm.  
DR InterPro; IPR003885; LRR\_Cyst.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR typ.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00041; fn3; 1.

DR Pfam; PF01463; LRRCT; 1.  
DR Pfam; PF01462; LRRNT; 1.  
DR Pfam; PF00560; LRR 1; 6.  
DR PRINTS; PR00019; LEURICHRPT.  
DR SMART; SM00181; EGF; 1.  
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DR SMART; SM00013; LRRNT; 1.  
DR SMART; SM00365; LRR SD22; 4.  
DR SMART; SM00369; LRR\_TVP; 8.  
DR PROSITE; PS00022; EGF 1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00026; EGF 3; 1.  
DR PROSITE; PS00853; FN3; 1.  
SQ SEQUENCE 673 AA; 71712 MW; 891E149652DEA286 CRC64;  
Query Match 98.2%; Score 3078.5; DB 2; Length 673;  
Best Local Similarity 88.6%; Pred. No. 28-165; 2; Indels 75; Gaps 1;  
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Db 1 MCSRVPPLLLPLLLALLGPGVQCGSCGSCSQPQTVFCTAROGTTVPRDVPDPTVGLYVF 60  
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Db 61 ENGITWLDAGSPAGLQGLDLSQNIASLPVGFQPLANLSNLDLTANRLHEITNPTF 120  
QY 91 ----- 180  
Db 121 RGLRLRLRYLGNKRIRHIQPGAFDTLDRLLKLQDNELRALPRLRLLLDLSHNS 180  
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Db 181 LLALEPGILDANVEALRLAGLGLQQLDEGLFRLRLNHLHDLDVSDNQLERVPVIRGLRG 240  
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RESULT 4  
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ID Q96CX1 HUMAN PRELIMINARY; PRT; 601 AA.  
AC Q96CX1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Slit12 protein (fragment)
GN Name=Slit12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
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RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013767; AAH13767.1; -; mRNA.
DR HSSP; Q9BZR6; 1P8T.
DR Ensembl; ENSG00000168140; Homo sapiens.
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DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF 1.
DR Pfam; PF00041; fn3 1.
DR Pfam; PF01463; LRCT; 1.
DR Pfam; PF00560; LRR 1; 6.
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DR SMART; SM00181; EGF 1.
DR SMART; SM00060; FN3 1.
DR SMART; SM00082; LRCT; 1.
DR SMART; SM00369; LRR_Typ; 2.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS00853; FN3 1.
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FT NON_TER
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Query Match 86.0%; Score 2697.5; DB 2; Length 601;
Best Local Similarity 87.4%; Pred. No. 5.4e-144;
Matches 525; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 73 AGLPGLQLDLDSQNIQAS-----90
DB 1 AGLPGLQLDLDSQNIQASLPVGQFPLANSLDLTANRLHEITNFTFGLRLRLRYLG 60

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DE membrane lipoprotein lipid attachment site/Cysteine-rich flanking  
 DE region, N-terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich  
 DE repeat, typical subtype/Leucine-rich repeat, outliers/Cysteine-rich  
 DE flanking region, C-terminal/Leucine-rich region/Fibronectin type III  
 DE domain containing protein, full insert sequence.  
 GN Names-Slit12;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
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 RN [1]  
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 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleschmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Mateu Y., Nikaudo I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Maghina J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RA The PANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Katsuna T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).

RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 RA Matsumoto T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Sakai K.,  
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Shiraki T.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK012169; BAB28075.1; -; mRNA.  
 DR HSSP; P00740; 1EDM.  
 DR Ensembl; ENSMUSG00000039646; Mus musculus.  
 DR MGI; MGI:217851; Slit12.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR Cterm.  
 DR InterPro; IPR000372; LRR Nterm.  
 DR InterPro; IPR003591; LRR typ.  
 DR Pfam; PF00008; EGF\_1.  
 DR Pfam; PF00041; fn3\_1.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR Pfam; PF00560; LRR\_1; 6.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR typ; 3.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS00853; FN3; 1.  
 KW Hypothetical protein; lipoprotein.  
 SQ SEQUENCE 673 AA; 72336 MW; 9C53F90ADF43PBD9 CRC64;  
 Query Match 79.2%; Score 2484; DB 2; Length 673;  
 Best Local Similarity 73.4%; Pred. No. 6.6e-132;  
 Matches 490; Conservative 25; Mismatches 75; Indels 78; Gaps 3;  
 QY 6 PLLLLPLLLLLALPGVQCGQCPGCGCQCPQVFTCTARQGTTPVDPVPPDTPVGLVYPENGIT 65  
 DB 9 PLL--LLLLLVLLSGVQCGQCPGCGCQCPQVFTCTARQGTTPVDPVPPDTPVGLVYPENGIT 66  
 QY 66 MLDASSFAGLPGQLQLDLSQNIAS-----LRLPLLLDLSHNSLLALE 110  
 DB 67 TLDVCGFAGLPGQLQLDLSQNIASLPGGIFQPLVNLNLDLTANKLHEISNTRFGLRR 126  
 QY 91 -----LRLPLLLDLSHNSLLALE 110  
 DB 127 LERLYLGNRIHRIHQGFADLRLLLEKLPDNEURVLPPLHLPRLLDLSDHNSIPALE 186  
 QY 111 PGILDTANVEALRLAGLQQLDEGLFSRLRNLDHLDVSDNOLERVPPVIRGLGLTRLR 170  
 DB 187 AGILDTANVEALRLAGLQQLDEGLFGRLLNLDHLDVYDQLEHMPSVIQGLGLTRLR 246  
 QY 171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDSLGLFPRLRLAAARNPNCVCP 230  
 DB 247 LAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSLFPRLRLAAARNPNCVCP 306  
 QY 231 LSWFGPWVREHVTLASPEETRTCHPPPPKAGLLELDYADFGCCPATTTTATVTPTRPV 290  
 DB 307 LSWFGPWVREHVTLASPEETRTCHPPPPKAGLLELDYADFGCCPATTTTATVTPTRV 366











DT 01-MAR-2003 (TEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)  
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)  
 DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length  
 DE enriched library, clone:A530098L04 product:KIAA0405 (FIBRONECTIN leucine rich  
 DE REPEAT TRANSMEMBRANE PROTEIN FLRT2) homolog (Fibronectin leucine rich  
 DE transmembrane protein 2).  
 GN Name=Map4k5; Synonyms=1f2;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_taxid=1009p;  
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 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.;  
 RA "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Officelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring K., Ringwald C., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RL "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 [4]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 [5]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka T., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6xCBA;  
 RC Haines B.P., Summerbell D., Rigby P.W.J.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 [8]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=FVB/N;  
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old  
 RC virgin mouse. Taken by biopsy.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Stailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [9]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=FVB/N;  
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old  
 RC virgin mouse. Taken by biopsy.  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK041311; BAC30900.1; -; mRNA.  
 DR EMBL: AV495669; AAR92202.1; -; mRNA.  
 DR EMBL: BC096471; AAN96471.1; -; mRNA.  
 DR HSSP: P07359; IM0Z.  
 DR Ensembl: ENSMUSG00000047414; Mus musculus.  
 DR MGI: MGI:1925503; Map4k5.  
 DR GO: GO:0016021; C: integral to membrane; IEA.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR Cterm.  
 DR InterPro: IPR000372; LRR Nterm.  
 DR InterPro: IPR003591; LRR typ.  
 DR InterPro: IPR001211; PhospholipaseA2.  
 DR Pfam: PF00041; fn3; 1.  
 DR Pfam: PF00560; LRR1; 8.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.



RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kiseunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RA "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima T., Kondo S., Konno H., Kouda M., Koya S.,  
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 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RL [7]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima T., Kondo S., Konno H., Kouda M., Koya S.,  
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 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AK048678; BAC33419.1; -; mRNA.  
 DR EMBL; AK078176; BAC37163.1; -; mRNA.  
 DR HSP; Q9BZ86; 10ZN.  
 DR Ensembl; ENSMUSG00000033707; Mus musculus.  
 DR MGI; MGI:2445060; Lrrc14.  
 DR GO; GO:0004180; F:carboxypeptidase activity; IEA.  
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00560; LRR\_1; 4.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00408; ICG2; 1.  
 DR SMART; SM00369; LRR\_TYP; 3.  
 DR SMART; SM00082; LRRCT; 1.  
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Query Match 10.8%; Score 339; DB 2; Length 521;  
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 Matches 149; Conservative 66; Mismatches 217; Indels 120; Gaps 21;  
 QY 1 MCSRVPLLLPL---LLLLALGPGV-----QCGSGGCGCQSQPQTVCTARQTTVPRDVPDP 53  
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 DB 120 GLRGAFVGLVQLRVLYLAGNLAKLLDFTFLHLPLQLHLQENSIE----- 167  
 QY 167 TRLRLAGNTRIAQLRPEDLAGLAQLDELVDNLSLQALPGDSLGLPRLRLLLAAANPFN 226  
 DB 168 -----LLEDQALAGLSLALLDLRLNQLGTISKALQPLSLQLVRLTENPWR 215  
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 DB 216 CDCALHWLGSWIKEGRRLLSRDKKITCAEPRLALQSLLEVSGLSIC-----IP 267  
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 QY 388 SLTLGI-EPVSPSTSLRVGLQRLVQSSVQLRSRLTYRNLSPGDKKLVTL----- 436  
 DB 375 QOSQQLPDQAPATRPVGHEPQHEAGSMAFRALGLATOTAITAATLALTALLAAMIC 434  
 QY 437 -----RLPASLAEYT-----VTQLRPNATYSVCVM-----PLGPGRVPE 470  
 DB 435 RRRRRKKVPAPSGSGTLFVNDYSDGCTTFAQLLELRDDHGHMFVDRSKPLFPPEVLP- 493  
 QY 471 GEEACGEAHTPP 482  
 DB 494 -EEA--PEHNPP 502  
 Search completed: February 7, 2006, 16:17:42  
 Job time : 283 secs

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OM protein - protein search, using sw model

Run on: February 7, 2006, 16:21:46 ; Search time 49 Seconds  
(without alignments)  
1008.981 Million cell updates/sec

Title: US-10-677-669-69

Perfect score: 3135

Sequence: 1 MCSRVELLPPLLLLLALGPG.....PLMGFPGGLQSLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCUTS COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3135	100.0	598	2	US-09-944-457-69
3	3135	100.0	598	2	US-09-945-584-69
4	3135	100.0	598	2	US-09-944-944-69
5	3135	100.0	598	2	US-09-945-587-69
6	3083.5	98.4	673	2	US-09-063-950-2
7	3083.5	98.4	673	2	US-09-991-181-52
8	3083.5	98.4	673	2	US-09-990-444-52
9	3083.5	98.4	673	2	US-09-997-333-52
10	3083.5	98.4	673	2	US-09-992-598-52
11	337	10.7	653	2	US-09-520-781-10
12	337	10.7	653	2	US-09-957-187-10
13	337	10.7	653	2	US-09-991-053-10
14	333	10.6	590	2	US-09-520-781-12
15	333	10.6	590	2	US-09-957-187-12
16	333	10.6	590	2	US-09-991-053-12
17	330	10.5	653	2	US-09-991-181-229
18	330	10.5	653	2	US-09-990-444-229
19	330	10.5	653	2	US-09-997-333-229
20	330	10.5	653	2	US-09-992-598-229
21	322	10.3	605	2	US-09-063-950-5
22	320	10.2	660	2	US-09-907-794A-28
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24	320	10.2	660	2	US-09-902-775A-28
25	320	10.2	660	2	US-09-906-700-28
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27	320	10.2	660	2	US-09-904-920A-28
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56	292.5	9.3	640	2	US-09-905-125A-292
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75	287.5	9.2	713	2	US-09-906-700-245
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95	271	8.6	473	2	US-10-020-445A-400
96	259	8.3	610	1	US-07-821-717B-6
97	259	8.3	610	1	US-08-119-262B-6
98	259	8.3	610	1	US-08-135-929A-11
99	259	8.3	610	1	US-08-234-265A-11
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102	258	8.2	1523	2	US-10-015-389A-198	Sequence 198, App	175	211	6.7	513	2	US-10-011-833A-385	Sequence 385, App
103	258	8.2	1523	2	US-10-006-768A-198	Sequence 198, App	176	211	6.7	513	2	US-10-006-041A-385	Sequence 385, App
104	258	8.2	1523	2	US-10-015-671A-198	Sequence 198, App	177	211	6.7	513	2	US-10-012-064A-385	Sequence 385, App
105	258	8.2	1523	2	US-10-011-393A-198	Sequence 198, App	178	210.5	6.7	4302	2	US-08-658-136-5	Sequence 5, Appli
106	258	8.2	1523	2	US-10-011-833A-198	Sequence 198, App	179	210.5	6.7	4302	2	US-09-053-469-8	Sequence 8, Appli
107	258	8.2	1523	2	US-10-006-041A-198	Sequence 198, App	180	210.5	6.7	4302	2	US-08-422-582-8	Sequence 8, Appli
108	258	8.2	1523	2	US-10-012-064A-198	Sequence 198, App	181	210.5	6.7	4302	2	US-09-052-282-8	Sequence 8, Appli
109	255.5	8.1	1480	2	US-09-191-647-7	Sequence 7, Appli	182	209	6.7	353	2	US-10-012-231A-397	Sequence 397, App
110	255.5	8.1	1480	2	US-09-540-245A-7	Sequence 7, Appli	183	209	6.7	353	2	US-10-015-389A-397	Sequence 397, App
111	255.5	8.1	1480	2	US-09-540-153-7	Sequence 7, Appli	184	209	6.7	353	2	US-10-006-768A-397	Sequence 397, App
112	255.5	8.1	1480	2	US-09-182-024A-5	Sequence 5, Appli	185	209	6.7	353	2	US-10-015-671A-397	Sequence 397, App
113	255.5	8.1	1480	2	US-10-289-776-7	Sequence 7, Appli	186	209	6.7	353	2	US-10-015-393A-397	Sequence 397, App
114	255.5	8.1	1480	4	PCT-US91-09055-2	Sequence 2, Appli	187	209	6.7	353	2	US-10-011-833A-397	Sequence 397, App
115	253	8.1	567	2	US-10-037-417-106	Sequence 106, App	188	209	6.7	353	2	US-10-006-041A-397	Sequence 397, App
116	252	8.0	567	2	US-09-775-803-12	Sequence 12, Appl	189	209	6.7	353	2	US-10-012-064A-397	Sequence 397, App
117	252	8.0	567	2	US-10-037-417-105	Sequence 105, App	190	209	6.7	1091	2	US-08-986-485-5	Sequence 5, Appli
118	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appl	191	208.5	6.7	424	2	US-09-949-016-7950	Sequence 7950, Ap
119	249.5	8.0	789	2	US-09-831-846-2	Sequence 2, Appli	192	207.5	6.6	415	2	US-09-949-016-7950	Sequence 7950, Ap
120	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appli	193	207.5	6.6	440	2	US-09-935-430-659	Sequence 659, App
121	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, Ap	194	207.5	6.6	440	2	US-09-964-956-29	Sequence 29, Appl
122	247.5	7.9	1525	2	US-09-191-647-2	Sequence 2, Appli	195	207.5	6.6	798	2	US-09-935-430-658	Sequence 658, App
123	247.5	7.9	1525	2	US-09-540-245A-2	Sequence 2, Appli	196	206.5	6.6	798	2	US-09-964-956-28	Sequence 28, Appl
124	247.5	7.9	1525	2	US-09-540-153-2	Sequence 2, Appli	197	206	6.6	1101	2	US-08-986-485-2	Sequence 2, Appli
125	247.5	7.9	1525	2	US-10-289-776-2	Sequence 2, Appli	198	206	6.6	428	2	US-09-949-016-6625	Sequence 6625, Ap
126	247.5	7.9	1529	2	US-10-188-495-67	Sequence 67, Appl	199	205	6.6	433	2	US-09-949-016-8521	Sequence 8521, Ap
127	246.5	7.9	1529	2	US-09-312-283C-396	Sequence 396, App	200	205	6.5	4339	2	US-09-052-469-6	Sequence 6, Appli
128	244	7.8	708	2	US-09-131-648-2	Sequence 2, Appli	201	205	6.5	4339	2	US-08-422-582-6	Sequence 6, Appli
129	244	7.8	708	2	US-09-907-794A-69	Sequence 69, Appl	202	203.5	6.5	4303	1	US-08-460-751-2	Sequence 2, Appli
130	244	7.8	708	2	US-09-905-125A-69	Sequence 69, Appl	203	203.5	6.5	4303	2	US-09-479-467A-2	Sequence 2, Appli
131	244	7.8	708	2	US-09-902-775A-69	Sequence 69, Appl	204	203.5	6.5	4303	2	US-09-655-160-2	Sequence 2, Appli
132	244	7.8	708	2	US-09-906-700-69	Sequence 69, Appl	205	200.5	6.4	302	2	US-09-482-273-105	Sequence 105, App
133	244	7.8	708	2	US-09-903-603A-69	Sequence 69, Appl	206	200.5	6.4	724	2	US-10-104-047-2224	Sequence 2224, Ap
134	244	7.8	708	2	US-09-904-920A-69	Sequence 69, Appl	207	199	6.3	3231	2	US-10-104-047-2504	Sequence 2504, Ap
135	244	7.8	708	2	US-09-909-064-69	Sequence 69, Appl	208	198.5	6.3	1338	2	US-09-631-603-2	Sequence 2, Appli
136	244	7.8	708	2	US-09-905-381A-69	Sequence 69, Appl	209	197.5	6.3	616	2	US-10-012-231A-24	Sequence 24, Appl
137	244	7.8	708	2	US-09-906-618-69	Sequence 69, Appl	210	197.5	6.3	616	2	US-10-015-389A-24	Sequence 24, Appl
138	244	7.8	708	2	US-09-906-646-69	Sequence 69, Appl	211	197.5	6.3	616	2	US-10-006-768A-24	Sequence 24, Appl
139	244	7.8	708	2	US-09-904-462-69	Sequence 69, Appl	212	197.5	6.3	616	2	US-10-015-671A-24	Sequence 24, Appl
140	244	7.8	708	2	US-09-902-736A-69	Sequence 69, Appl	213	197.5	6.3	616	2	US-10-015-393A-24	Sequence 24, Appl
141	244	7.8	708	2	US-09-906-722A-69	Sequence 69, Appl	214	197.5	6.3	616	2	US-10-011-833A-24	Sequence 24, Appl
142	243.5	7.8	312	2	US-10-037-417-108	Sequence 108, App	215	197.5	6.3	616	2	US-10-006-041A-24	Sequence 24, Appl
143	241	7.7	380	2	US-09-461-325-161	Sequence 161, App	216	197.5	6.3	616	2	US-10-012-064A-24	Sequence 24, Appl
144	241	7.7	380	2	US-10-012-542-161	Sequence 161, App	217	196.5	6.3	716	2	US-09-312-283C-183	Sequence 183, App
145	241	7.7	380	2	US-10-115-123-161	Sequence 161, App	218	196.5	6.3	771	2	US-09-188-930-183	Sequence 183, App
146	240	7.7	560	2	US-08-592-500-2	Sequence 2, Appli	219	195.5	6.2	553	2	US-10-037-417-28	Sequence 28, Appl
147	240	7.7	560	2	US-08-195-006-2	Sequence 2, Appli	220	195	6.2	620	2	US-09-907-794A-73	Sequence 73, Appl
148	240	7.7	560	2	US-09-063-950-4	Sequence 4, Appli	221	195	6.2	620	2	US-09-905-125A-73	Sequence 73, Appl
149	240	7.7	560	2	US-09-775-803-14	Sequence 14, Appl	222	195	6.2	620	2	US-09-902-775A-73	Sequence 73, Appl
150	240	7.7	560	4	PCT-US94-07644A-2	Sequence 2, Appli	223	195	6.2	620	2	US-09-906-700-73	Sequence 73, Appl
151	236.5	7.5	222	4	PCT-US91-09055-3	Sequence 3, Appli	224	195	6.2	620	2	US-09-903-603A-73	Sequence 73, Appl
152	236.5	7.5	231	2	US-08-986-485-7	Sequence 7, Appli	225	195	6.2	620	2	US-09-904-920A-73	Sequence 73, Appl
153	227	7.2	568	2	US-10-673-245-14	Sequence 14, Appl	226	195	6.2	620	2	US-09-909-064-73	Sequence 73, Appl
154	226.5	7.2	557	2	US-10-037-417-95	Sequence 95, Appl	227	195	6.2	620	2	US-09-905-381A-73	Sequence 73, Appl
155	225	7.2	735	2	US-09-191-647-9	Sequence 9, Appli	228	195	6.2	620	2	US-09-906-618-73	Sequence 73, Appl
156	225	7.2	735	2	US-09-540-245A-9	Sequence 9, Appli	229	195	6.2	620	2	US-09-906-646-73	Sequence 73, Appl
157	225	7.2	735	2	US-09-540-153-9	Sequence 9, Appli	230	195	6.2	620	2	US-09-904-462-73	Sequence 73, Appl
158	225	7.2	735	2	US-10-289-776-9	Sequence 9, Appli	231	195	6.2	620	2	US-09-906-722A-73	Sequence 73, Appl
159	222.5	7.1	536	2	US-09-538-092-992	Sequence 992, App	232	195	6.2	620	2	US-09-906-736A-73	Sequence 73, Appl
160	222	7.1	196	4	PCT-US91-09055-5	Sequence 5, Appli	233	195	6.2	742	2	US-10-104-047-2807	Sequence 2807, Ap
161	222	7.1	498	2	US-10-188-495-51	Sequence 51, Appl	234	195	6.2	832	2	US-09-935-430-660	Sequence 660, App
162	222	7.1	591	2	US-10-188-495-50	Sequence 50, Appl	235	195	6.2	853	2	US-09-964-956-30	Sequence 30, Appl
163	221.5	7.1	557	2	US-10-188-495-50	Sequence 50, Appl	236	194.5	6.2	699	2	US-09-949-016-6073	Sequence 6073, Ap
164	220.5	7.0	841	2	US-09-935-4310-94	Sequence 94, Appl	237	194.5	6.2	720	2	US-09-949-016-9819	Sequence 9819, Ap
165	218.5	7.0	841	2	US-09-964-956-2	Sequence 2, Appli	238	193.5	6.2	242	4	PCT-US91-09055-4	Sequence 4, Appli
166	218.5	7.0	359	2	US-09-949-016-9732	Sequence 9732, Ap	239	193.5	6.2	542	2	US-10-037-417-97	Sequence 97, Appl
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168	217.5	6.8	837	2	US-09-964-956-5	Sequence 5, Appli	241	190	6.1	1059	2	US-09-905-125A-290	Sequence 290, App
169	214.5	6.8	255	2	US-09-893-737-232	Sequence 232, App	242	190	6.1	1059	2	US-09-902-775A-290	Sequence 290, App
170	211	6.7	513	2	US-10-012-231A-385	Sequence 385, App	243	190	6.1	1059	2	US-09-906-700-290	Sequence 290, App
171	211	6.7	513	2	US-10-015-389A-385	Sequence 385, App	244	190	6.1	1059	2	US-09-903-603A-290	Sequence 290, App
172	211	6.7	513	2	US-10-006-768A-385	Sequence 385, App	245	190	6.1	1059	2	US-09-904-920A-290	Sequence 290, App
173	211	6.7	513	2	US-10-015-671A-385	Sequence 385, App	246	190	6.1	1059	2	US-09-905-064-290	Sequence 290, App

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248	190	6.1	1059	2	US-09-906-618-290	Sequence 290, App	321	167	5.3	1112	2	US-09-353-585-3	Sequence 3, Appli
249	190	6.1	1059	2	US-09-906-646-290	Sequence 290, App	322	166.5	5.3	224	2	US-09-482-273-174	Sequence 174, App
250	190	6.1	1059	2	US-09-904-462-290	Sequence 290, App	323	166	5.3	1112	2	US-09-353-585-2	Sequence 2, Appli
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252	190	6.1	1059	2	US-09-906-722A-290	Sequence 290, App	325	164.5	5.2	501	2	US-09-905-125A-185	Sequence 185, App
253	190	6.1	1119	2	US-09-907-794A-290	Sequence 294, App	326	164.5	5.2	501	2	US-09-902-775A-185	Sequence 185, App
254	190	6.1	1119	2	US-09-905-125A-294	Sequence 294, App	327	164.5	5.2	501	2	US-09-906-700-185	Sequence 185, App
255	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App	328	164.5	5.2	501	2	US-09-903-603A-185	Sequence 185, App
256	190	6.1	1119	2	US-09-906-700-294	Sequence 294, App	329	164.5	5.2	501	2	US-09-904-620A-185	Sequence 185, App
257	190	6.1	1119	2	US-09-903-603A-294	Sequence 294, App	330	164.5	5.2	501	2	US-09-909-064-185	Sequence 185, App
258	190	6.1	1119	2	US-09-904-920A-294	Sequence 294, App	331	164.5	5.2	501	2	US-09-905-381A-185	Sequence 185, App
259	190	6.1	1119	2	US-09-909-064-294	Sequence 294, App	332	164.5	5.2	501	2	US-09-906-618-185	Sequence 185, App
260	190	6.1	1119	2	US-09-905-381A-294	Sequence 294, App	333	164.5	5.2	501	2	US-09-906-646-185	Sequence 185, App
261	190	6.1	1119	2	US-09-906-618-294	Sequence 294, App	334	164.5	5.2	501	2	US-09-904-462-185	Sequence 185, App
262	190	6.1	1119	2	US-09-906-646-294	Sequence 294, App	335	164.5	5.2	501	2	US-09-902-736A-185	Sequence 185, App
263	190	6.1	1119	2	US-09-904-462-294	Sequence 294, App	336	164.5	5.2	501	2	US-09-906-722A-185	Sequence 185, App
264	190	6.1	1119	2	US-09-902-736A-294	Sequence 294, App	337	164.5	5.2	582	2	US-09-081-149-8	Sequence 8, Appli
265	190	6.1	1119	2	US-09-906-722A-294	Sequence 294, App	338	164.5	5.2	584	2	US-09-949-016-10752	Sequence 10752, A
266	186.5	5.9	196	4	PCT-US91-09055-6	Sequence 6, Appli	339	164.5	5.2	858	2	US-10-104-047-2918	Sequence 2918, Ap
267	186.5	5.9	844	2	US-09-538-092-999	Sequence 938, Ap	340	164	5.2	696	2	US-09-907-794A-91	Sequence 91, Appl
268	186	5.9	440	2	US-09-949-016-9438	Sequence 999, App	341	164	5.2	696	2	US-09-905-125A-91	Sequence 91, Appl
269	186	5.9	451	2	US-09-949-016-9282	Sequence 9282, Ap	342	164	5.2	696	2	US-09-902-775A-91	Sequence 91, Appl
270	184	5.9	320	1	US-07-613-083B-1	Sequence 1, Appli	343	164	5.2	696	2	US-09-906-700-91	Sequence 91, Appl
271	184	5.9	368	2	US-09-949-016-6115	Sequence 6115, Ap	344	164	5.2	696	2	US-09-903-603A-91	Sequence 91, Appl
272	184	5.9	368	2	US-09-715-836A-9	Sequence 9, Appli	345	164	5.2	696	2	US-09-904-920A-91	Sequence 91, Appl
273	184	5.9	382	2	US-09-949-016-10542	Sequence 10542, A	346	164	5.2	696	2	US-09-909-064-91	Sequence 91, Appl
274	183	5.8	662	2	US-09-538-092-1325	Sequence 1325, Ap	347	164	5.2	696	2	US-09-905-381A-91	Sequence 91, Appl
275	183	5.8	662	2	US-09-949-016-6319	Sequence 6319, Ap	348	164	5.2	696	2	US-09-906-618-91	Sequence 91, Appl
276	183	5.8	665	2	US-09-949-016-10710	Sequence 10710, A	349	164	5.2	696	2	US-09-906-646-91	Sequence 91, Appl
277	182.5	5.8	379	2	US-09-866-028-2	Sequence 2, Appli	350	164	5.2	696	2	US-09-904-462-91	Sequence 91, Appl
278	182.5	5.8	379	2	US-09-944-457-2	Sequence 2, Appli	351	164	5.2	696	2	US-09-902-736A-91	Sequence 91, Appl
279	182.5	5.8	379	2	US-09-945-584-2	Sequence 2, Appli	352	164	5.2	696	2	US-09-906-722A-91	Sequence 91, Appl
280	182.5	5.8	379	2	US-09-944-944-2	Sequence 2, Appli	353	164	5.2	904	2	US-09-949-002-352	Sequence 352, App
281	182.5	5.8	379	2	US-09-945-587-2	Sequence 2, Appli	354	164	5.2	910	2	US-09-949-002-483	Sequence 483, App
282	182.5	5.8	958	2	US-09-706-594-5	Sequence 5, Appli	355	163	5.2	753	2	US-09-081-149-7	Sequence 7, Appli
283	182.5	5.8	966	2	US-09-964-956-32	Sequence 32, Appli	356	163	5.2	782	2	US-09-056-383-13	Sequence 13, Appli
284	182	5.8	378	2	US-09-689-486-62	Sequence 62, Appli	357	161	5.1	559	2	US-09-081-149-2	Sequence 2, Appli
285	180	5.7	493	2	US-10-037-417-30	Sequence 30, App	358	160	5.1	942	2	US-10-101-464A-911	Sequence 911, App
286	180	5.7	989	2	US-09-954-987B-171	Sequence 171, App	359	158.5	5.1	1032	2	US-09-954-987B-192	Sequence 192, App
287	178	5.7	368	1	US-08-303-238-3	Sequence 3, Appli	360	158	5.0	257	2	US-09-270-767-41554	Sequence 41554, A
288	178	5.7	368	1	US-08-458-834-3	Sequence 3, Appli	361	158	5.0	352	2	US-09-949-016-6781	Sequence 6781, Ap
289	178	5.7	522	2	US-09-991-181-278	Sequence 278, App	362	158	5.0	374	2	US-09-949-016-7689	Sequence 7689, Ap
290	178	5.7	522	2	US-09-990-444-278	Sequence 278, App	363	157.5	5.0	236	1	US-08-443-063A-42	Sequence 42, Appl
291	178	5.7	522	2	US-09-997-333-278	Sequence 278, App	364	157.5	5.0	672	2	US-09-949-002-522	Sequence 522, App
292	178	5.7	522	2	US-09-992-598-278	Sequence 278, App	365	157	5.0	796	2	US-10-104-047-2293	Sequence 2293, Ap
293	178	5.7	1049	2	US-09-999-833A-496	Sequence 496, App	366	156.5	5.0	376	2	US-09-538-092-1276	Sequence 1276, Ap
294	178	5.7	1049	2	US-09-954-987B-170	Sequence 170, App	367	156	5.0	975	2	US-09-949-016-7595	Sequence 7595, Ap
295	178	5.7	1049	2	US-10-020-445A-496	Sequence 496, App	368	155	4.9	1041	2	US-09-999-833A-498	Sequence 498, App
296	178	5.7	1052	2	US-09-949-016-11508	Sequence 11508, A	369	155	4.9	1041	2	US-09-954-987B-184	Sequence 184, App
297	177.5	5.7	1050	2	US-09-954-987B-175	Sequence 175, App	370	155	4.9	1041	2	US-09-954-987B-186	Sequence 186, App
298	176.5	5.6	522	2	US-10-104-047-2664	Sequence 2664, Ap	371	155	4.9	1041	2	US-10-020-445A-498	Sequence 498, App
299	175	5.6	368	6	5340934-2	Patent No. 5340934	372	155	4.9	1059	2	US-09-954-987B-187	Sequence 187, App
300	173.5	5.5	998	2	US-10-101-464A-914	Sequence 914, App	373	154.5	4.9	377	2	US-09-949-016-7949	Sequence 7949, Ap
301	172.5	5.5	282	1	US-08-442-063A-45	Sequence 45, Appl	374	154.5	4.9	1495	2	US-08-522-736B-1	Sequence 1, Appli
302	172.5	5.5	307	1	US-08-442-063A-48	Sequence 48, Appl	375	154.5	4.9	894	1	US-09-337-384-1	Sequence 1, Appli
303	172.5	5.5	333	1	US-08-442-063A-27	Sequence 27, Appl	376	153.5	4.9	894	1	US-08-372-892-2	Sequence 2, Appli
304	172.5	5.5	338	2	US-09-689-486-63	Sequence 63, Appl	377	153.5	4.9	894	1	US-08-445-640-34	Sequence 34, Appl
305	172.5	5.5	342	1	US-08-272-919-2	Sequence 2, Appli	378	153.5	4.9	894	2	US-08-170-558-34	Sequence 34, Appl
306	172.5	5.5	342	1	US-08-619-916-2	Sequence 2, Appli	379	153.5	4.9	894	2	US-08-447-314-34	Sequence 34, Appl
307	172.5	5.5	342	4	PCT-US95-08542-2	Sequence 2, Appli	380	153.5	4.9	894	2	US-08-445-461-34	Sequence 34, Appl
308	172.5	5.5	359	1	US-08-303-238-4	Sequence 4, Appli	381	153.5	4.9	894	2	US-09-223-490-34	Sequence 34, Appl
309	172.5	5.5	359	2	US-08-458-834-4	Sequence 4, Appli	382	153.5	4.9	1032	2	US-09-954-987B-5	Sequence 6, Appli
310	172.5	5.5	359	2	US-09-538-092-868	Sequence 868, App	383	153	4.9	679	2	US-09-252-991A-18857	Sequence 18857, A
311	172.5	5.5	359	2	US-09-949-016-6143	Sequence 6143, Ap	384	153	4.9	699	2	US-10-237-551-143	Sequence 143, App
312	172.5	5.5	360	2	US-09-949-016-7925	Sequence 7925, Ap	385	153	4.9	699	2	US-10-237-551-254	Sequence 254, App
313	172.5	5.5	1388	2	US-10-153-469A-10	Sequence 10, Appl	386	153	4.9	1248	2	US-10-042-810-2	Sequence 2, Appli
314	172.5	5.5	1388	2	US-10-104-889-10	Sequence 10, Appl	387	153	4.9	1278	2	US-10-042-810-4	Sequence 4, Appli
315	170.5	5.4	373	2	US-09-724-864-43	Sequence 43, Appl	388	152.5	4.9	364	2	US-10-104-047-2127	Sequence 2127, Ap
316	170	5.4	907	2	US-09-170-496D-264	Sequence 264, App	389	152	4.8	786	2	US-09-949-002-351	Sequence 351, App
317	170	5.4	907	2	US-09-170-496D-278	Sequence 278, App	390	152	4.8	796	2	US-09-949-002-386	Sequence 386, App
318	169.5	5.4	353	6	5340934-4	Patent No. 5340934	391	152	4.8	802	2	US-09-949-002-512	Sequence 512, App
319	168	5.4	1049	2	US-09-954-987B-172	Sequence 172, App	392	151.5	4.8	455	2	US-10-188-495-3	Sequence 3, Appli

393	151.5	4.8	1564	2	US-09-467-997-1	Sequence 1, Appli	466	138.5	4.4	811	2	US-09-997-333-57	Sequence 57, Appl
394	151	4.8	532	2	US-09-270-767-46234	Sequence 46234, A	467	138.5	4.4	811	2	US-09-992-598-57	Sequence 57, Appl
395	150.5	4.8	695	1	US-08-487-886-2	Sequence 2, Appli	468	138	4.4	323	2	US-09-949-016-7924	Sequence 7924, Ap
396	150.5	4.8	695	2	US-08-482-855-2	Sequence 2, Appli	469	137.5	4.4	141	2	US-09-270-767-45511	Sequence 45511, A
397	150.5	4.8	695	2	US-08-474-986-2	GENERAL INFO	470	137.5	4.4	884	6	5208144-8	Patent No. 5208144
398	150	4.8	259	2	US-09-907-794A-71	Sequence 71, Appl	471	137	4.4	4544	1	US-08-469-486-52	Sequence 52, Appl
399	150	4.8	259	2	US-09-905-125A-71	Sequence 71, Appl	472	137	4.4	4544	1	US-08-469-658-52	Sequence 52, Appl
400	150	4.8	259	2	US-09-902-775A-71	Sequence 71, Appl	473	136.5	4.4	984	2	US-10-101-464A-919	Sequence 919, App
401	150	4.8	259	2	US-09-906-700-71	Sequence 71, Appl	474	136.5	4.4	2972	2	US-09-579-181-2	Sequence 2, Appli
402	150	4.8	259	2	US-09-903-603A-71	Sequence 71, Appl	475	136.5	4.4	3118	2	US-09-579-181-1	Sequence 1, Appli
403	150	4.8	259	2	US-09-904-920A-71	Sequence 71, Appl	476	136	4.3	287	2	US-10-104-047-3292	Sequence 3292, Ap
404	150	4.8	259	2	US-09-909-064-71	Sequence 71, Appl	477	136	4.3	692	2	US-07-757-342D-6	Sequence 6, Appli
405	150	4.8	259	2	US-09-905-381A-71	Sequence 71, Appl	478	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appli
406	150	4.8	259	2	US-09-906-618-71	Sequence 71, Appl	479	135.5	4.3	536	2	US-09-252-931A-31124	Sequence 31124, A
407	150	4.8	259	2	US-09-906-646-71	Sequence 71, Appl	480	135.5	4.3	743	2	US-09-771-161A-164	Sequence 164, App
408	150	4.8	259	2	US-09-904-462-71	Sequence 71, Appl	481	135.5	4.3	743	2	US-09-771-161A-254	Sequence 254, App
409	150	4.8	259	2	US-09-902-736A-71	Sequence 71, Appl	482	135	4.3	446	2	US-10-101-464A-733	Sequence 733, App
410	150	4.8	259	2	US-09-906-722A-71	Sequence 71, Appl	483	135	4.3	538	2	US-09-616-289-43	Sequence 43, Appl
411	150	4.8	513	2	US-09-068-804-14	Sequence 14, Appl	484	135	4.3	538	2	US-09-976-740-43	Sequence 43, Appl
412	149	4.8	503	2	US-10-037-417-104	Sequence 104, App	485	135	4.3	723	2	US-09-434-048-2	Sequence 2, Appli
413	149	4.8	1012	1	US-08-475-891A-4	Sequence 4, Appli	486	135	4.3	723	2	US-10-104-047-2572	Sequence 2572, Ap
414	149	4.8	1025	1	US-08-567-375-4	Sequence 4, Appli	487	135	4.3	907	2	US-08-783-774-2	Sequence 2, Appli
415	149	4.8	1025	1	US-08-587-680A-4	Sequence 4, Appli	488	135	4.3	907	2	US-09-328-599A-1	Sequence 1, Appli
416	149	4.8	1026	2	US-09-623-551-18	Sequence 18, Appl	489	135	4.3	807	4	PCT-US95-04611A-19	Sequence 19, Appl
417	149	4.8	1026	2	US-09-364-206-2	Sequence 2, Appli	490	134.5	4.3	802	2	US-09-823-240A-2	Sequence 2, Appli
418	149	4.8	1874	2	US-09-331-403-2	Sequence 2, Appli	491	134	4.3	536	2	US-09-292-225-21	Sequence 21, Appl
419	148.5	4.7	375	1	US-08-303-238-2	Sequence 2, Appli	492	134	4.3	550	2	US-09-616-289-47	Sequence 47, Appl
420	148.5	4.7	375	1	US-08-458-834-2	Sequence 2, Appli	493	134	4.3	550	2	US-09-976-740-47	Sequence 47, Appl
421	147.5	4.7	570	2	US-09-565-501A-104	Sequence 104, App	494	134	4.3	555	2	US-09-292-225-15	Sequence 15, Appl
422	147.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App	495	134	4.3	555	2	US-09-292-225-18	Sequence 18, Appl
423	147.5	4.7	570	2	US-09-874-923-104	Sequence 104, App	496	133.5	4.3	1166	2	US-10-101-464A-900	Sequence 900, App
424	147.5	4.7	1728	2	US-09-949-002-532	Sequence 532, App	497	133	4.2	652	2	US-10-104-047-3364	Sequence 3364, Ap
425	147	4.7	177	2	US-09-270-767-32705	Sequence 32705, A	498	133	4.2	4391	2	US-10-006-011A-2	Sequence 2, Appli
426	147	4.7	177	2	US-09-270-767-47922	Sequence 47922, A	499	132.5	4.2	390	2	US-08-460-576-2	Sequence 2, Appli
427	147	4.7	265	2	US-09-270-767-45056	Sequence 45056, A	500	132.5	4.2	463	1	US-08-162-402B-9	Sequence 9, Appli
428	147	4.7	214	1	US-08-227-536-2	Sequence 2, Appli	501	132.5	4.2	579	2	US-09-325-932A-185	Sequence 185, App
429	147	4.7	214	1	US-09-538-092-1289	Sequence 1289, Ap	502	132.5	4.2	583	2	US-09-641-612-2	Sequence 2, Appli
430	147	4.7	214	4	PCT-US95-04682-2	Sequence 2, Appli	503	132.5	4.2	2035	1	US-08-046-585-5	Sequence 5, Appli
431	146.5	4.7	325	2	US-10-104-047-3320	Sequence 3320, Ap	504	132.5	4.2	2035	1	US-08-393-703-5	Sequence 5, Appli
432	146.5	4.7	344	2	US-10-104-047-3358	Sequence 3358, Ap	505	132.5	4.2	2035	4	PCT-US93-11721-5	Sequence 5, Appli
433	146.5	4.7	1404	1	US-08-400-159-2	Sequence 2, Appli	506	132.5	4.2	2045	2	US-09-949-016-10491	Sequence 10491, A
434	146.5	4.7	1404	1	US-08-611-729A-2	Sequence 2, Appli	507	132.5	4.2	3122	2	US-10-237-551-201	Sequence 201, App
435	146.5	4.7	1404	2	US-09-195-524-2	Sequence 2, Appli	508	132.5	4.2	3122	2	US-10-237-551-250	Sequence 250, App
436	146	4.7	786	2	US-09-103-429A-3	Sequence 3, Appli	509	132	4.2	287	2	US-09-893-737-110	Sequence 110, App
437	146	4.7	788	2	US-09-294-663-3	Sequence 3, Appli	510	132	4.2	465	1	US-08-162-402B-8	Sequence 8, Appli
438	146	4.7	885	1	US-08-372-892-4	Sequence 4, Appli	511	132	4.2	705	2	US-10-101-464A-894	Sequence 894, App
439	146	4.7	885	2	US-09-919-497-52	Sequence 52, Appli	512	132	4.2	979	2	US-08-514-213A-2	Sequence 2, Appli
440	145.5	4.6	2142	2	US-09-538-092-1142	Sequence 1142, Ap	513	132	4.2	979	2	US-09-015-399-5	Sequence 5, Appli
441	145.5	4.6	2142	2	US-09-949-002-371	Sequence 371, App	514	132	4.2	1003	2	US-09-949-016-11260	Sequence 11260, A
442	145	4.6	353	2	US-09-949-016-7923	Sequence 7923, Ap	515	131.5	4.2	461	2	US-10-037-417-96	Sequence 96, Appl
443	145	4.6	1032	2	US-09-954-987B-3	Sequence 3, Appli	516	131.5	4.2	571	2	US-09-252-991A-30533	Sequence 30533, A
444	144	4.6	661	1	US-08-514-014-4	Sequence 4, Appli	517	131	4.2	180	2	US-08-986-485-8	Sequence 8, Appli
445	144	4.6	661	1	US-08-833-823-4	Sequence 4, Appli	518	131	4.2	227	2	US-10-101-464A-666	Sequence 666, App
446	143.5	4.6	1274	2	US-09-095-443-2	Sequence 2, Appli	519	131	4.2	279	2	US-09-270-767-41558	Sequence 41558, A
447	143	4.6	935	2	US-09-477-962-107	Sequence 107, App	520	131	4.2	407	2	US-09-270-767-46649	Sequence 6, Appli
448	142.5	4.5	141	2	US-09-270-767-31706	Sequence 31706, A	521	131	4.2	799	2	US-09-180-439-6	Sequence 6, Appli
449	142.5	4.5	141	2	US-09-270-767-46923	Sequence 46923, A	522	131	4.2	947	2	US-09-228-986-73	Sequence 73, Appl
450	142.5	4.5	805	2	US-09-103-429A-4	Sequence 4, Appli	523	131	4.2	947	2	US-10-101-464A-73	Sequence 73, Appl
451	142.5	4.5	807	2	US-09-294-663-4	Sequence 4, Appli	524	131	4.2	1062	2	US-09-902-540-16313	Sequence 16313, A
452	142	4.5	326	2	US-09-689-486-64	Sequence 64, Appl	525	131	4.2	1196	2	US-08-881-706-2	Sequence 2, Appli
453	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appli	526	131	4.2	1196	2	US-09-823-394-2	Sequence 2, Appli
454	142	4.5	365	2	US-10-101-464A-901	Sequence 901, App	527	131	4.2	1938	2	US-09-949-016-6609	Sequence 6609, Ap
455	142	4.5	435	2	US-10-188-495-5	Sequence 5, Appli	528	130.5	4.2	843	2	US-10-101-464A-893	Sequence 893, App
456	142	4.5	661	2	US-10-037-417-107	Sequence 107, App	529	130.5	4.2	878	2	US-09-556-706B-2	Sequence 2, Appli
457	140.5	4.5	345	2	US-10-101-464A-802	Sequence 802, App	530	130.5	4.2	3729	1	US-09-724-418A-2	Sequence 2, Appli
458	140.5	4.5	376	1	US-08-303-238-1	Sequence 1, Appli	531	130.5	4.2	878	2	US-08-804-227C-4	Sequence 4, Appli
459	140.5	4.5	376	2	US-08-458-834-1	Sequence 1, Appli	532	130	4.1	619	2	US-10-037-417-34	Sequence 34, Appl
460	140	4.5	283	2	US-09-949-016-7910	Sequence 7910, Ap	533	130	4.1	645	2	US-10-101-464A-920	Sequence 920, App
461	140	4.5	547	2	US-10-101-464A-928	Sequence 928, App	534	129.5	4.1	550	2	US-09-252-991A-21295	Sequence 21295, A
462	139	4.4	5179	2	US-09-538-092-1258	Sequence 1258, Ap	535	129.5	4.1	912	4	PCT-US95-03747-2	Sequence 2, Appli
463	138.5	4.4	710	2	US-10-104-047-3402	Sequence 3402, Ap	536	129	4.1	363	2	US-09-270-767-44030	Sequence 44030, A
464	138.5	4.4	811	2	US-09-991-181-57	Sequence 57, Appl	537	129	4.1	823	2	US-09-252-991A-23655	Sequence 23655, A
465	138.5	4.4	811	2	US-09-990-444-57	Sequence 57, Appl	538	129	4.1	885	2	US-09-252-991A-26129	Sequence 26129, A

539	129	4.1	1133	2	US-10-101-464A-809	Sequence 809, App	612	124.5	4.0	546	2	US-09-906-700-250	Sequence 250, App
540	129	4.1	1940	1	US-08-644-271-30	Sequence 30, Appl	613	124.5	4.0	546	2	US-09-903-603A-250	Sequence 250, App
541	129	4.1	1940	2	US-09-077-955-34	Sequence 34, Appl	614	124.5	4.0	546	2	US-09-904-920A-250	Sequence 250, App
542	129	4.1	1940	2	US-10-016-283-34	Sequence 34, Appl	615	124.5	4.0	546	2	US-09-909-064-250	Sequence 250, App
543	129	4.1	2321	2	US-09-230-652-2	Sequence 2, Appl	616	124.5	4.0	546	2	US-09-905-381A-250	Sequence 250, App
544	128.5	4.1	188	1	US-08-442-063A-39	Sequence 39, Appl	617	124.5	4.0	546	2	US-09-906-618-250	Sequence 250, App
545	128.5	4.1	446	1	US-08-836-854-15	Sequence 15, Appl	618	124.5	4.0	546	2	US-09-906-646-250	Sequence 250, App
546	128.5	4.1	508	2	US-10-104-047-3233	Sequence 3233, Ap	619	124.5	4.0	546	2	US-09-904-462-250	Sequence 250, App
547	128.5	4.1	653	2	US-10-101-464A-953	Sequence 953, App	620	124.5	4.0	546	2	US-09-902-736A-250	Sequence 250, App
548	128.5	4.1	864	2	US-10-101-464A-896	Sequence 896, App	621	124.5	4.0	546	2	US-09-906-722A-250	Sequence 250, App
549	128.5	4.1	865	2	US-09-902-540-10416	Sequence 10416, A	622	124.5	4.0	623	2	US-09-949-016-6530	Sequence 6530, Ap
550	128.5	4.1	1023	1	US-08-475-891A-2	Sequence 2, Appl	623	124.5	4.0	998	2	US-10-101-464A-895	Sequence 895, App
551	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appl	624	124.5	4.0	1042	2	US-09-252-991A-3044	Sequence 3044, A
552	128.5	4.1	1023	1	US-08-587-680A-2	Sequence 2, Appl	625	124.5	4.0	1709	2	US-09-949-016-10503	Sequence 10503, A
553	128	4.1	475	2	US-09-252-991A-30242	Sequence 30242, A	626	124	4.0	277	2	US-07-741-453A-58	Sequence 58, Appl
554	128	4.1	538	1	US-08-541-759B-2	Sequence 2, Appl	627	124	4.0	707	2	US-09-228-986-80	Sequence 80, Appl
555	128	4.1	717	2	US-10-101-464A-810	Sequence 810, App	628	124	4.0	707	2	US-10-101-464A-80	Sequence 80, Appl
556	127.5	4.1	1006	2	US-10-415-147-12	Sequence 12, Appl	629	124	4.0	1457	2	US-08-665-253-27	Sequence 27, Appl
557	127.5	4.1	1522	2	US-10-144-198-31	Sequence 31, Appl	630	124	4.0	1457	2	US-08-762-500-27	Sequence 27, Appl
558	127.5	4.1	1581	2	US-09-949-002-414	Sequence 414, App	631	124	4.0	1472	2	US-09-032-438C-119	Sequence 119, App
559	127.5	4.1	3969	2	US-08-061-376-5	Sequence 5, Appl	632	123.5	3.9	1312	2	US-09-041-886-19	Sequence 19, App
560	127.5	4.1	3969	2	US-09-538-092-1262	Sequence 1262, Ap	633	123.5	3.9	1312	2	US-09-648-281-2	Sequence 2, Appl
561	127	4.1	260	2	US-09-270-767-32658	Sequence 32658, A	634	123.5	3.9	1312	2	US-09-707-919A-19	Sequence 19, Appl
562	127	4.1	615	2	US-09-252-991A-26695	Sequence 26695, A	635	123.5	3.9	1312	2	US-09-083-268-3	Sequence 3, Appl
563	126.5	4.0	141	2	US-09-270-767-32244	Sequence 32244, A	636	123.5	3.9	1312	2	US-08-981-998A-3	Sequence 3, Appl
564	126.5	4.0	141	2	US-09-270-767-47461	Sequence 47461, A	637	123	3.9	383	2	US-10-101-464A-898	Sequence 898, App
565	126.5	4.0	438	2	US-09-991-181-129	Sequence 129, App	638	123	3.9	526	2	US-09-252-991A-23688	Sequence 23688, A
566	126.5	4.0	438	2	US-09-990-444-129	Sequence 129, App	639	123	3.9	557	2	US-09-248-796A-26892	Sequence 26892, A
567	126.5	4.0	438	2	US-09-997-333-129	Sequence 129, App	640	123	3.9	888	1	US-08-445-640-35	Sequence 35, Appl
568	126.5	4.0	438	2	US-09-992-598-129	Sequence 129, App	641	123	3.9	888	2	US-08-170-558-35	Sequence 35, Appl
569	126.5	4.0	659	2	US-09-423-753-3	Sequence 3, Appl	642	123	3.9	888	2	US-08-447-314-35	Sequence 35, Appl
570	126.5	4.0	685	2	US-08-872-855-2	Sequence 2, Appl	643	123	3.9	888	2	US-08-445-461-35	Sequence 35, Appl
571	126.5	4.0	685	2	US-09-423-753-25	Sequence 25, Appl	644	123	3.9	888	2	US-09-223-490-35	Sequence 35, Appl
572	126.5	4.0	685	2	US-09-641-612-7	Sequence 7, Appl	645	123	3.9	924	1	US-08-481-130-28	Sequence 28, Appl
573	126.5	4.0	919	2	US-10-101-464A-642	Sequence 642, App	646	123	3.9	924	1	US-08-656-984A-28	Sequence 28, Appl
574	126.5	4.0	999	1	US-08-473-553A-5	Sequence 5, Appl	647	123	3.9	924	1	US-08-485-604-28	Sequence 28, Appl
575	126	4.0	143	2	US-09-893-737-190	Sequence 190, App	648	123	3.9	924	1	US-08-487-595-28	Sequence 28, Appl
576	126	4.0	152	2	US-09-270-767-33594	Sequence 33594, A	649	122.5	3.9	494	2	US-09-248-796A-16546	Sequence 16546, A
577	126	4.0	775	2	US-09-949-016-8799	Sequence 8799, Ap	650	122.5	3.9	595	2	US-09-641-612-5	Sequence 5, Appl
578	126	4.0	1485	2	US-09-762-569-4	Sequence 4, Appl	651	122.5	3.9	596	2	US-09-252-991A-18875	Sequence 18875, A
579	126	4.0	1821	2	US-09-949-016-5938	Sequence 5938, Ap	652	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl
580	125.5	4.0	258	2	US-10-012-231A-153	Sequence 153, App	653	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl
581	125.5	4.0	258	2	US-10-015-389A-153	Sequence 153, App	654	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl
582	125.5	4.0	258	2	US-10-006-768A-153	Sequence 153, App	655	122.5	3.9	1036	2	US-09-771-161A-255	Sequence 255, App
583	125.5	4.0	258	2	US-10-015-671A-153	Sequence 153, App	656	122.5	3.9	1036	2	US-09-771-161A-256	Sequence 256, App
584	125.5	4.0	258	2	US-10-015-393A-153	Sequence 153, App	657	122	3.9	191	2	US-09-461-325-186	Sequence 186, App
585	125.5	4.0	258	2	US-10-011-833A-153	Sequence 153, App	658	122	3.9	191	2	US-10-012-542-186	Sequence 186, App
586	125.5	4.0	258	2	US-10-006-041A-153	Sequence 153, App	659	122	3.9	191	2	US-10-115-123-186	Sequence 186, App
587	125.5	4.0	258	2	US-10-012-064A-153	Sequence 153, App	660	122	3.9	206	2	US-09-461-325-412	Sequence 412, App
588	125.5	4.0	440	2	US-08-985-335-3	Sequence 3, Appl	661	122	3.9	206	2	US-10-115-123-412	Sequence 412, App
589	125.5	4.0	440	2	US-09-410-372-3	Sequence 3, Appl	662	122	3.9	312	2	US-09-270-767-31750	Sequence 31750, A
590	125.5	4.0	764	2	US-07-741-453A-54	Sequence 54, Appl	663	122	3.9	328	1	US-08-414-928A-9	Sequence 9, Appl
591	125.5	4.0	764	2	US-07-741-453A-60	Sequence 60, Appl	664	122	3.9	328	1	US-08-926-922-9	Sequence 9, Appl
592	125.5	4.0	1129	2	US-09-023-905A-2	Sequence 2, Appl	665	122	3.9	328	1	US-09-253-682-9	Sequence 9, Appl
593	125	4.0	419	2	US-10-002-344A-237	Sequence 237, App	666	122	3.9	328	2	US-09-527-657-9	Sequence 9, Appl
594	125	4.0	757	2	US-09-252-991A-25918	Sequence 25918, A	667	122	3.9	328	2	US-09-892-100-9	Sequence 9, Appl
595	125	4.0	957	2	US-09-252-991A-20408	Sequence 20408, A	668	122	3.9	481	2	US-09-949-016-9748	Sequence 9748, Ap
596	125	4.0	1139	2	US-09-513-505-2	Sequence 2, Appl	669	122	3.9	495	2	US-09-252-991A-31949	Sequence 31949, A
597	125	4.0	2023	2	US-09-491-356C-8	Sequence 8, Appl	670	122	3.9	515	2	US-09-252-991A-28127	Sequence 28127, A
598	125	4.0	2126	2	US-09-487-558B-86	Sequence 86, Appl	671	122	3.9	515	2	US-09-370-838-216	Sequence 216, App
599	125	4.0	2126	2	US-09-538-092-1377	Sequence 1377, Ap	672	122	3.9	527	2	US-09-854-133-216	Sequence 216, App
600	125	4.0	2294	2	US-09-252-991A-17231	Sequence 17231, A	673	122	3.9	529	2	US-09-716-9648-2	Sequence 2, Appl
601	124.5	4.0	107	2	US-09-270-767-61021	Sequence 61021, A	674	122	3.9	320	2	US-09-325-932A-190	Sequence 190, App
602	124.5	4.0	298	2	US-09-232-160-17	Sequence 17, Appl	675	121.5	3.9	477	2	US-09-252-991A-19831	Sequence 19831, A
603	124.5	4.0	298	2	US-09-800-723-87	Sequence 87, Appl	676	121.5	3.9	695	2	US-09-248-796A-18020	Sequence 18020, A
604	124.5	4.0	298	2	US-09-800-723-121	Sequence 121, App	677	121.5	3.9	818	2	US-10-104-047-2546	Sequence 2546, Ap
605	124.5	4.0	298	2	US-10-000-489-22	Sequence 22, Appl	678	121.5	3.9	1225	2	US-09-501-171-4	Sequence 4, Appl
606	124.5	4.0	298	2	US-09-832-129-50	Sequence 50, App	679	121.5	3.9	1225	2	US-09-949-016-6063	Sequence 6063, Ap
607	124.5	4.0	307	2	US-09-949-016-9817	Sequence 9817, Ap	680	121.5	3.9	1251	4	PCT-US95-02251-3	Sequence 3, Appl
608	124.5	4.0	307	2	US-09-949-016-9818	Sequence 9818, Ap	681	121.5	3.9	1251	4	US-08-199-780-3	Sequence 3, Appl
609	124.5	4.0	546	2	US-09-907-794A-250	Sequence 250, App	682	121.5	3.9	1252	1	US-08-316-650-3	Sequence 3, Appl
610	124.5	4.0	546	2	US-09-905-125A-250	Sequence 250, App	683	121.5	3.9	1252	1	US-08-479-722B-4	Sequence 4, Appl
611	124.5	4.0	546	2	US-09-902-775A-250	Sequence 250, App	684	121.5	3.9	1253	2		

685	121.5	3.9	1253	2	US-09-592-685-4	Sequence 4, Appli	758	117.5	3.7	190	1	US-08-441-629-4	Sequence 4, Appli
686	121	3.9	499	2	US-09-049-672A-1	Sequence 1, Appli	759	117.5	3.7	190	2	US-08-776-207-4	Sequence 4, Appli
687	121	3.9	739	2	US-09-902-540-10606	Sequence 10606, A	760	117.5	3.7	190	2	US-09-507-773-4	Sequence 4, Appli
688	121	3.9	910	2	US-09-228-986-72	Sequence 72, Appl	761	117.5	3.7	190	2	US-10-016-447-4	Sequence 4, Appli
689	121	3.9	910	2	US-10-101-464A-72	Sequence 72, Appl	762	117.5	3.7	190	4	PCT-US95-09172-4	Sequence 4, Appli
690	121	3.9	1139	2	US-09-513-505-4	Sequence 4, Appli	763	117.5	3.7	247	2	US-10-101-464A-730	Sequence 730, App
691	120.5	3.8	141	1	US-08-442-063A-36	Sequence 36, Appl	764	117.5	3.7	563	2	US-09-252-991A-17549	Sequence 17549, A
692	120.5	3.8	426	2	US-09-252-991A-24450	Sequence 24450, A	765	117.5	3.7	635	1	US-08-484-101B-36	Sequence 36, Appl
693	120.5	3.8	464	2	US-09-716-964B-4	Sequence 4, Appli	766	117.5	3.7	635	1	US-08-484-101B-50	Sequence 50, Appl
694	120.5	3.8	562	2	US-09-902-540-13269	Sequence 13269, A	767	117.5	3.7	635	2	US-08-714-524D-36	Sequence 36, Appl
695	120.5	3.8	787	2	US-09-721-383-2	Sequence 2, Appli	768	117.5	3.7	635	2	US-08-714-524D-50	Sequence 50, Appl
696	120.5	3.8	787	2	US-09-721-137-2	Sequence 2, Appli	769	117.5	3.7	996	2	US-10-101-464A-889	Sequence 889, App
697	120.5	3.8	787	2	US-09-721-251-2	Sequence 2, Appli	770	117.5	3.7	996	2	US-10-101-464A-933	Sequence 933, App
698	120.5	3.8	787	2	US-10-114-764-2	Sequence 2, Appli	771	117.5	3.7	1118	1	US-09-252-991A-24340	Sequence 24340, A
699	120.5	3.8	988	2	US-10-101-464A-931	Sequence 931, App	772	117.5	3.7	1706	1	US-08-459-568-2	Sequence 2, Appli
700	120.5	3.8	1104	2	US-09-981-953A-4	Sequence 4, Appli	773	117.5	3.7	1706	1	US-08-399-411-2	Sequence 2, Appli
701	120.5	3.8	1587	2	US-09-949-002-354	Sequence 354, App	774	117.5	3.7	1706	2	US-08-516-859A-2	Sequence 2, Appli
702	120.5	3.8	1610	2	US-09-548-473B-4	Sequence 4, Appli	775	117.5	3.7	1706	2	US-09-586-472-2	Sequence 2, Appli
703	120.5	3.8	1665	2	US-09-858-664A-2	Sequence 2, Appli	776	117.5	3.7	1706	2	US-09-528-706-2	Sequence 2, Appli
704	120.5	3.8	1665	2	US-10-274-978-2	Sequence 2, Appli	777	117.5	3.7	1706	2	US-10-024-450-2	Sequence 2, Appli
705	120.5	3.8	1665	2	US-10-697-263-2	Sequence 2, Appli	778	117	3.7	401	2	US-09-252-991A-32529	Sequence 32529, A
706	120.5	3.8	2396	2	US-09-548-473B-6	Sequence 6, Appli	779	117	3.7	655	1	US-08-148-910-12	Sequence 12, Appl
707	120	3.8	130	2	US-09-270-767-33086	Sequence 33086, A	780	117	3.7	655	1	US-08-448-937A-12	Sequence 12, Appl
708	120	3.8	467	2	US-09-046-736-2	Sequence 48303, A	781	117	3.7	809	2	US-09-252-991A-31759	Sequence 31759, A
709	120	3.8	523	1	US-08-473-553A-3	Sequence 3, Appli	782	117	3.7	888	2	US-09-252-991A-23787	Sequence 23787, A
710	120	3.8	569	2	US-09-514-245-22	Sequence 22, Appl	783	117	3.7	980	1	US-08-473-553A-6	Sequence 6, Appli
711	120	3.8	603	2	US-09-506-779-4	Sequence 4, Appli	784	117	3.7	985	1	US-08-473-553A-2	Sequence 2, Appli
712	120	3.8	696	2	US-09-758-759-125	Sequence 125, App	785	117	3.7	1055	2	US-09-214-278-2	Sequence 2, Appli
713	120	3.8	2556	1	US-08-185-432-17	Sequence 17, Appl	786	117	3.7	1055	2	US-09-855-722-2	Sequence 2, Appli
714	120	3.8	2556	2	US-08-899-232-2	Sequence 2, Appli	787	117	3.7	1148	2	US-08-882-046-4	Sequence 4, Appli
715	120	3.8	2556	2	US-09-121-457-2	Sequence 2, Appli	788	117	3.7	1148	2	US-09-566-047-4	Sequence 4, Appli
716	120	3.8	2556	2	US-09-107-433-3721	Sequence 3721, Ap	789	117	3.7	1193	1	US-08-400-159-10	Sequence 10, Appl
717	119.5	3.8	608	2	US-09-949-016-11148	Sequence 11148, A	790	117	3.7	1193	2	US-08-611-729A-10	Sequence 10, Appl
718	119.5	3.8	608	2	US-09-949-016-11149	Sequence 11149, A	791	117	3.7	1193	2	US-09-195-524-10	Sequence 10, Appl
719	119.5	3.8	608	2	US-09-949-016-11150	Sequence 11150, A	792	117	3.7	1193	2	US-09-310-685-8	Sequence 8, Appli
720	119.5	3.8	608	2	US-09-949-016-11151	Sequence 11151, A	793	117	3.7	1212	2	US-09-214-278-3	Sequence 3, Appli
721	119.5	3.8	1034	2	US-09-252-991A-28921	Sequence 28921, A	794	117	3.7	1212	2	US-09-855-722-3	Sequence 3, Appli
722	119.5	3.8	1034	2	US-09-171-699-10	Sequence 10, Appl	795	117	3.7	1238	2	US-09-855-722-5	Sequence 5, Appli
723	119.5	3.8	1048	2	US-08-560-005-5	Sequence 5, Appli	796	117	3.7	1238	2	US-08-611-729A-8	Sequence 8, Appli
724	119.5	3.8	1149	2	US-09-418-540-5	Sequence 5, Appli	797	117	3.7	1257	2	US-09-195-524-8	Sequence 8, Appli
725	119.5	3.8	1149	2	US-09-969-528-5	Sequence 5, Appli	798	117	3.7	1257	2	US-09-310-685-6	Sequence 6, Appli
726	119.5	3.8	1596	2	US-10-101-464A-717	Sequence 717, App	799	117	3.7	132	2	US-10-101-464A-572	Sequence 572, App
727	119.5	3.8	304	2	US-09-538-092-887	Sequence 887, App	800	116.5	3.7	296	2	US-09-270-767-37980	Sequence 37980, A
728	119	3.8	319	2	US-08-630-172-12	Sequence 12, Appl	801	116.5	3.7	296	2	US-09-270-767-53197	Sequence 53197, A
729	119	3.8	319	2	US-09-375-419-12	Sequence 12, Appl	802	116.5	3.7	439	2	US-10-300-819B-21	Sequence 21, Appl
730	119	3.8	528	2	US-08-928-213B-8	Sequence 8, Appli	803	116.5	3.7	943	2	US-08-476-515A-12	Sequence 12, Appl
731	119	3.8	593	2	US-09-252-991A-20441	Sequence 20441, A	804	116.5	3.7	944	2	US-08-652-877-12	Sequence 12, Appl
732	119	3.8	784	2	US-09-982-308B-23	Sequence 23, Appl	805	116.5	3.7	1252	2	US-09-902-540-13967	Sequence 13967, A
733	119	3.8	1081	2	US-09-369-364A-17	Sequence 17, Appl	806	116.5	3.7	2887	2	US-08-462-467B-8	Sequence 8, Appli
734	119	3.8	1721	2	US-09-270-767-43049	Sequence 43049, A	807	116.5	3.7	4654	2	US-08-476-515A-84	Sequence 84, Appli
735	118.5	3.8	422	2	US-09-949-016-8251	Sequence 8251, Ap	808	116.5	3.7	4655	2	US-08-652-877-84	Sequence 84, Appl
736	118.5	3.8	430	2	US-09-949-016-8782	Sequence 8782, Ap	809	116.5	3.7	4655	2	US-08-652-877-86	Sequence 86, Appl
737	118.5	3.8	486	1	US-08-450-360-2	Sequence 2, Appli	810	116.5	3.7	4655	2	US-08-652-877-88	Sequence 88, Appl
738	118.5	3.8	883	2	US-10-188-495-72	Sequence 72, Appl	811	116.5	3.7	4655	2	US-08-652-877-90	Sequence 90, Appl
739	118.5	3.8	1166	2	US-08-317-310A-64	Sequence 64, Appl	812	116.5	3.7	193	2	US-09-270-767-44942	Sequence 44942, A
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741	118.5	3.8	149	2	US-09-270-767-47835	Sequence 47835, A	814	116	3.7	1053	2	US-09-513-505-8	Sequence 8, Appli
742	118	3.8	462	2	US-09-252-991A-20814	Sequence 20814, A	815	116	3.7	1181	2	US-09-826-509-587	Sequence 587, App
743	118	3.8	947	2	US-09-252-991A-21335	Sequence 21335, A	816	116	3.7	1291	2	US-09-150-460B-10	Sequence 10, Appl
744	118	3.8	1044	2	US-09-252-991A-18853	Sequence 18853, A	817	116	3.7	1291	2	US-09-220-641-5	Sequence 5, Appli
745	118	3.8	1064	2	US-09-252-991A-17508	Sequence 17508, A	818	116	3.7	1291	2	US-09-548-473B-1	Sequence 1, Appli
746	118	3.8	1084	2	US-10-071-900-3	Sequence 3, Appli	819	116	3.7	1351	2	US-08-083-550A-20	Sequence 20, Appl
747	118	3.8	1084	2	US-08-804-227C-3	Sequence 3, Appli	820	116	3.7	2556	1	US-08-532-384A-20	Sequence 20, Appl
748	118	3.8	1864	1	US-08-185-432-16	Sequence 16, Appl	821	116	3.7	138	2	US-09-191-647-4	Sequence 4, Appli
749	118	3.8	2471	1	US-08-083-590A-19	Sequence 19, Appl	822	115.5	3.7	138	2	US-09-540-245A-4	Sequence 4, Appli
750	118	3.8	2471	2	US-08-899-232-1	Sequence 1, Appli	823	115.5	3.7	138	2	US-10-289-776-4	Sequence 4, Appli
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837	115	3.7	1189	2	US-09-287-354-4	Sequence 4, Appli	910	113	3.6	1247	2	US-09-501-171-6	Sequence 6, Appli
838	115	3.7	1189	2	US-09-949-016-6931	Sequence 6931, Ap	911	112.5	3.6	328	2	US-09-252-991A-17729	Sequence 17729, A
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843	114.5	3.7	545	2	US-09-949-002-297	Sequence 297, App	916	112.5	3.6	694	2	US-09-949-016-8775	Sequence 8775, Ap
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851	114.5	3.7	935	2	US-09-302-540-16200	Sequence 16200, A	924	112	3.6	241	2	US-08-470-339-195	Sequence 195, App
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873	114.5	3.7	1218	2	US-09-949-016-5902	Sequence 5902, Ap	946	112	3.6	764	2	US-09-826-509-403	Sequence 403, App
874	114.5	3.7	1218	2	US-09-310-685-4	Sequence 4, Appli	947	112	3.6	764	2	US-09-826-509-407	Sequence 407, App
875	114.5	3.7	1254	2	US-09-949-016-10297	Sequence 10297, A	948	112	3.6	764	2	US-09-826-509-411	Sequence 411, App
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878	114	3.6	224	2	US-09-220-528-29	Sequence 29, Appl	951	112	3.6	764	2	US-09-826-509-423	Sequence 423, App
879	114	3.6	224	2	US-09-347-613C-16	Sequence 16, Appl	952	112	3.6	902	1	US-08-396-479B-6	Sequence 6, Appli
880	114	3.6	224	2	US-09-662-183A-16	Sequence 16, Appl	953	112	3.6	902	1	US-08-818-823-6	Sequence 6, Appli
881	114	3.6	257	2	US-10-101-464A-743	Sequence 743, App	954	112	3.6	990	2	US-10-101-464A-814	Sequence 814, App
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901	113.5	3.6	1218	2	US-09-855-722-7	Sequence 7, Appli	974	111	3.5	239	2	US-09-252-991A-21250	Sequence 21250, A
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903	113	3.6	369	2	US-09-252-991A-25394	Sequence 25394, A	976	111	3.5	267	2	US-08-818-111-137	Sequence 137, App

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978	111	3.5	267	2	US-09-072-596-137	Sequence 137, App	1051	109.5	3.5	343	2	US-10-101-464A-892	Sequence 892, App
979	111	3.5	267	2	US-09-072-967-142	Sequence 137, App	1052	109.5	3.5	381	2	US-10-101-464A-660	Sequence 660, App
980	111	3.5	267	2	US-10-193-002-137	Sequence 142, App	1053	109.5	3.5	400	2	US-10-101-464A-939	Sequence 939, App
981	111	3.5	267	2	US-10-084-843-142	Sequence 142, App	1054	109.5	3.5	401	6	5252556-1	Patent No. 5252556
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983	111	3.5	333	2	US-09-252-991A-19956	Sequence 19956, A	1056	109.5	3.5	456	2	US-08-467-602-303	Sequence 303, App
984	111	3.5	452	2	US-09-949-016-7289	Sequence 7289, App	1057	109.5	3.5	456	2	US-08-411-295F-229	Sequence 229, App
985	111	3.5	454	2	US-09-716-964B-5	Sequence 5, App11	1058	109.5	3.5	490	2	US-08-467-602-345	Sequence 345, App
986	111	3.5	492	1	US-08-644-271-32	Sequence 32, App1	1059	109.5	3.5	490	2	US-08-411-295F-271	Sequence 271, App
987	111	3.5	492	2	US-09-077-955-36	Sequence 36, App1	1060	109.5	3.5	612	1	US-08-359-705B-8	Sequence 8, App11
988	111	3.5	492	2	US-10-016-283-36	Sequence 36, App1	1061	109.5	3.5	612	1	US-08-286-846A-8	Sequence 8, App11
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995	111	3.5	1318	2	US-10-237-551-197	Sequence 197, App	1068	109.5	3.5	690	2	US-10-101-464A-69	Sequence 69, App1
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997	111	3.5	1358	1	US-08-404-671-4	Sequence 4, App11	1070	109.5	3.5	697	2	US-10-101-464A-940	Sequence 940, App
998	111	3.5	1358	1	US-08-404-781-4	Sequence 4, App11	1071	109.5	3.5	784	2	US-09-004-838-12	Sequence 12, App1
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1005	111	3.5	1719	2	US-09-586-472-4	Sequence 4, App11	1078	109.5	3.5	839	2	US-09-156-923-6	Sequence 6, App11
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1007	111	3.5	1719	2	US-10-024-450-4	Sequence 4, App11	1080	109.5	3.5	1235	2	US-09-949-016-8455	Sequence 8455, App
1008	111	3.5	254	2	US-09-949-016-9270	Sequence 9270, App	1081	109.5	3.5	1235	2	US-09-949-016-8456	Sequence 8456, App
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1011	111	3.5	2523	1	US-08-185-432-18	Sequence 18, App1	1084	109	3.5	221	1	US-08-659-235C-29	Sequence 29, App1
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1014	110.5	3.5	273	2	US-09-252-991A-30433	Sequence 30433, A	1087	109	3.5	416	2	US-09-601-478-4	Sequence 4, App11
1015	110.5	3.5	298	2	US-09-248-796A-26762	Sequence 26762, A	1088	109	3.5	433	2	US-09-252-991A-29241	Sequence 29241, A
1016	110.5	3.5	565	2	US-08-937-067-8	Sequence 8, App11	1089	109	3.5	437	1	US-08-136-119-2	Sequence 2, App11
1017	110.5	3.5	645	2	US-09-964-899-17	Sequence 17, App1	1090	109	3.5	437	1	US-08-481-814A-7	Sequence 7, App11
1018	110.5	3.5	675	2	US-09-332-063-2	Sequence 2, App11	1091	109	3.5	437	2	US-09-253-991A-32620	Sequence 32620, A
1019	110.5	3.5	675	2	US-09-332-063-3	Sequence 3, App11	1092	109	3.5	447	2	US-09-949-002-540	Sequence 540, App
1020	110.5	3.5	708	2	US-09-818-780-76	Sequence 76, App1	1093	109	3.5	480	1	US-08-480-229C-10	Sequence 10, App1
1021	110.5	3.5	728	2	US-09-252-991A-31891	Sequence 31891, A	1094	109	3.5	480	1	US-08-659-235C-10	Sequence 10, App1
1022	110.5	3.5	815	2	US-09-538-092-1300	Sequence 1300, App	1095	109	3.5	507	2	US-09-599-287A-24	Sequence 24, App1
1023	110.5	3.5	1207	2	US-10-098-600B-16	Sequence 16, App1	1096	109	3.5	507	2	US-10-078-547-24	Sequence 24, App1
1024	110.5	3.5	1346	2	US-09-949-002-376	Sequence 376, App	1097	109	3.5	510	2	US-09-253-991A-25076	Sequence 25076, A
1025	110.5	3.5	1346	2	US-09-320-878-4	Sequence 4, App11	1098	109	3.5	510	2	US-09-252-991A-23036	Sequence 23036, A
1026	110.5	3.5	1346	2	US-09-105-537-37	Sequence 37, App1	1099	109	3.5	560	2	US-09-252-991A-25999	Sequence 25999, A
1027	110.5	3.5	1346	2	US-09-141-908-5	Sequence 5, App11	1100	109	3.5	749	2	US-09-828-313-27	Sequence 27, App1
1028	110.5	3.5	1346	2	US-09-657-440-4	Sequence 4, App11	1101	109	3.5	762	1	US-08-642-255-114	Sequence 114, App
1029	110.5	3.5	1346	2	US-09-793-708-4	Sequence 4, App11	1102	109	3.5	762	1	US-08-397-633A-26	Sequence 26, App1
1030	110.5	3.5	1384	2	US-08-976-255-11	Sequence 11, App1	1103	109	3.5	764	2	US-09-186-350A-53	Sequence 53, App1
1031	110.5	3.5	1656	2	US-09-949-016-7247	Sequence 7247, App	1104	109	3.5	828	2	US-10-101-464A-934	Sequence 934, App
1032	110.5	3.5	2476	1	US-08-276-967-2	Sequence 2, App11	1105	109	3.5	833	1	US-08-264-534-6	Sequence 6, App11
1033	110.5	3.5	3724	1	US-08-804-198-4	Sequence 4, App11	1106	109	3.5	833	1	US-08-083-590A-2	Sequence 2, App11
1034	110.5	3.5	3724	1	US-09-105-537-6	Sequence 6, App11	1107	109	3.5	833	1	US-08-346-126-6	Sequence 6, App11
1035	110.5	3.5	11877	2	US-09-105-537-6	Sequence 6, App11	1108	109	3.5	833	1	US-08-346-126-6	Sequence 6, App11
1036	110	3.5	195	2	US-09-858-664A-11	Sequence 11, App1	1109	109	3.5	833	2	US-08-532-384-2	Sequence 2, App11
1037	110	3.5	195	2	US-10-274-978-12	Sequence 12, App1	1110	109	3.5	833	2	US-08-893-828-6	Sequence 6, App11
1038	110	3.5	195	2	US-10-697-263-12	Sequence 12, App1	1111	109	3.5	833	2	US-08-893-828-6	Sequence 6, App11
1039	110	3.5	426	2	US-09-369-364A-19	Sequence 19, App1	1112	109	3.5	850	1	US-08-286-305A-7	Sequence 7, App11
1040	110	3.5	626	2	US-09-345-473E-43	Sequence 43, App1	1113	109	3.5	850	1	US-08-441-104A-7	Sequence 7, App11
1041	110	3.5	626	2	US-09-862-027-43	Sequence 43, App1	1114	109	3.5	850	1	US-08-440-816A-7	Sequence 7, App11
1042	110	3.5	633	2	US-09-248-796A-18023	Sequence 18023, A	1115	109	3.5	850	2	US-09-417-381A-7	Sequence 7, App11
1043	110	3.5	739	2	US-09-035-648-24	Sequence 24, App1	1116	109	3.5	860	2	US-09-252-991A-28607	Sequence 28607, A
1044	110	3.5	739	2	US-09-001-951-24	Sequence 24, App1	1117	109	3.5	883	2	US-10-193-970-3	Sequence 3, App11
1045	110	3.5	739	2	US-08-818-829-24	Sequence 24, App1	1118	109	3.5	883	2	US-10-193-970-6	Sequence 6, App11
1046	110	3.5	746	2	US-09-548-797B-4	Sequence 4, App11	1119	109	3.5	1145	2	US-09-758-759-167	Sequence 167, App
1047	110	3.5	2703	1	US-08-185-432-19	Sequence 19, App1	1120	109	3.5	1336	1	US-08-231-193A-58	Sequence 58, App1
1048	110	3.5	2703	2	US-08-899-232-4	Sequence 4, App11	1121	109	3.5	1336	1	US-08-486-273A-58	Sequence 58, App1
1049	110	3.5	2703	2	US-09-121-457-4	Sequence 4, App11	1122	109	3.5	1336	2	US-08-940-086A-58	Sequence 58, App1

1123	109	3.5	1336	2	US-08-940-035A-58	Sequence 58, Appl	1196	107.5	3.4	459	2	US-08-411-295F-225	Sequence 225, App
1124	109	3.5	1336	2	US-08-935-105A-58	Sequence 58, Appl	1197	107.5	3.4	493	2	US-08-467-602-341	Sequence 341, App
1125	109	3.5	1336	2	US-09-648-797-58	Sequence 58, Appl	1198	107.5	3.4	493	2	US-08-411-295F-267	Sequence 267, App
1126	109	3.5	1336	2	US-09-386-123-58	Sequence 58, Appl	1199	107.5	3.4	506	2	US-09-949-016-11282	Sequence 11282, A
1127	109	3.5	1336	2	US-10-038-937-58	Sequence 58, Appl	1200	107.5	3.4	520	2	US-09-068-740A-3	Sequence 3, Appl
1128	109	3.5	1336	2	US-10-007-747-58	Sequence 58, Appl	1201	107.5	3.4	568	2	US-09-252-991A-19968	Sequence 19968, A
1129	109	3.5	1336	2	US-09-945-901-58	Sequence 58, Appl	1202	107.5	3.4	655	1	US-07-736-178C-2	Sequence 2, Appl
1130	109	3.5	1358	2	US-09-949-002-353	Sequence 353, App	1203	107.5	3.4	660	2	US-10-101-464A-808	Sequence 808, App
1131	109	3.5	1385	2	US-09-949-002-431	Sequence 431, App	1204	107.5	3.4	691	2	US-09-252-991A-31413	Sequence 31413, A
1132	108.5	3.5	74	2	US-09-270-767-32762	Sequence 32762, A	1205	107.5	3.4	691	2	US-09-758-759-159	Sequence 159, App
1133	108.5	3.5	74	2	US-09-270-767-47979	Sequence 47979, A	1206	107.5	3.4	723	2	US-09-641-612-6	Sequence 6, Appl
1134	108.5	3.5	269	2	US-09-902-540-16596	Sequence 16596, A	1207	107.5	3.4	787	2	US-09-252-991A-19991	Sequence 19991, A
1135	108.5	3.5	288	2	US-09-902-540-16596	Sequence 16596, A	1208	107.5	3.4	832	2	US-08-981-392-6	Sequence 6, Appl
1136	108.5	3.5	381	2	US-09-510-031A-5	Sequence 5, Appl	1209	107.5	3.4	832	2	US-09-908-322-6	Sequence 6, Appl
1137	108.5	3.5	404	2	US-09-550-115-11	Sequence 11, Appl	1210	107.5	3.4	984	1	US-08-673-789-9	Sequence 9, Appl
1138	108.5	3.5	514	2	US-09-712-363-154	Sequence 154, App	1211	107.5	3.4	998	2	US-09-949-016-6695	Sequence 6695, Ap
1139	108.5	3.5	542	2	US-09-252-991A-21862	Sequence 21862, A	1212	107.5	3.4	1001	2	US-10-415-147-3	Sequence 3, Appl
1140	108.5	3.5	548	1	US-08-468-576B-19	Sequence 19, Appl	1213	107.5	3.4	1088	2	US-09-233-857-13	Sequence 13, Appl
1141	108.5	3.5	548	1	US-08-468-576B-19	Sequence 19, Appl	1214	107.5	3.4	1135	1	US-09-357-014-7	Sequence 7, Appl
1142	108.5	3.5	548	1	US-08-468-576B-19	Sequence 19, Appl	1215	107.5	3.4	1135	2	US-09-357-014-7	Sequence 7, Appl
1143	108.5	3.5	702	2	US-09-068-740A-4	Sequence 4, Appl	1216	107.5	3.4	1327	2	US-09-949-016-8412	Sequence 8412, Ap
1144	108.5	3.5	723	2	US-09-068-740A-4	Sequence 4, Appl	1217	107	3.4	131	1	US-08-650-598-3	Sequence 3, Appl
1145	108.5	3.5	723	2	US-09-423-753-27	Sequence 27, Appl	1218	107	3.4	232	2	US-09-149-476-623	Sequence 623, App
1146	108.5	3.5	825	1	US-07-912-952-2	Sequence 2, Appl	1219	107	3.4	288	2	US-09-252-991A-27676	Sequence 27676, A
1147	108.5	3.5	827	2	US-09-248-796A-17307	Sequence 17307, A	1220	107	3.4	354	2	US-09-949-016-6051	Sequence 6051, Ap
1148	108.5	3.5	904	2	US-09-252-991A-23202	Sequence 23202, A	1221	107	3.4	358	2	US-09-949-016-8148	Sequence 8148, Ap
1149	108.5	3.5	955	2	US-09-252-991A-24254	Sequence 24254, A	1222	107	3.4	360	2	US-09-248-796A-18991	Sequence 18991, A
1150	108.5	3.5	1125	2	US-09-513-783A-152	Sequence 152, App	1223	107	3.4	369	2	US-09-252-991A-29670	Sequence 29670, A
1151	108.5	3.5	1125	2	US-09-430-656-152	Sequence 152, App	1224	107	3.4	492	2	US-09-252-991A-23619	Sequence 23619, A
1152	108.5	3.5	1125	2	US-10-100-957A-112	Sequence 112, App	1225	107	3.4	500	2	US-09-423-753-2	Sequence 2, Appl
1153	108.5	3.5	1184	2	US-09-266-2250-18	Sequence 18, App	1226	107	3.4	541	2	US-10-101-464A-913	Sequence 913, App
1154	108.5	3.5	1527	2	US-09-695-795A-4	Sequence 4, Appl	1227	107	3.4	593	2	US-09-964-899-15	Sequence 15, Appl
1155	108.5	3.5	1610	2	US-09-513-783A-22	Sequence 22, Appl	1228	107	3.4	615	2	US-09-949-002-301	Sequence 301, App
1156	108.5	3.5	1610	2	US-09-430-656-22	Sequence 22, Appl	1229	107	3.4	759	2	US-09-252-991A-19071	Sequence 19071, A
1157	108.5	3.5	1610	2	US-10-100-957A-22	Sequence 22, Appl	1230	107	3.4	793	2	US-09-588-256-10	Sequence 256, A
1158	108	3.4	51	2	US-09-364-956-66	Sequence 66, Appl	1231	107	3.4	806	2	US-08-945-983-2	Sequence 2, Appl
1159	108	3.4	51	2	US-10-037-417-100	Sequence 100, App	1232	107	3.4	806	2	US-08-945-983-2	Sequence 2, Appl
1160	108	3.4	152	2	US-09-214-909-22	Sequence 22, Appl	1233	107	3.4	1241	2	US-08-714-741-34	Sequence 34, Appl
1161	108	3.4	180	2	US-09-133-341-12	Sequence 12, Appl	1234	107	3.4	1315	2	US-08-899-595-3	Sequence 3, Appl
1162	108	3.4	180	2	US-09-739-852-12	Sequence 12, Appl	1235	106.5	3.4	157	2	US-08-981-322-68	Sequence 68, Appl
1163	108	3.4	419	2	US-10-237-551-198	Sequence 198, App	1236	106.5	3.4	157	2	US-09-908-322-68	Sequence 68, Appl
1164	108	3.4	590	1	US-08-785-310A-5	Sequence 5, Appl	1237	106.5	3.4	157	2	US-09-310-685-20	Sequence 20, Appl
1165	108	3.4	618	2	US-09-252-991A-23373	Sequence 23373, A	1238	106.5	3.4	176	2	US-09-270-767-32581	Sequence 32581, A
1166	108	3.4	670	2	US-09-252-991A-32445	Sequence 32445, A	1239	106.5	3.4	176	2	US-09-270-767-47798	Sequence 47798, A
1167	108	3.4	703	2	US-09-367-206-5	Sequence 5, Appl	1240	106.5	3.4	247	2	US-09-252-991A-23672	Sequence 23672, A
1168	108	3.4	703	2	US-09-298-404-5	Sequence 5, Appl	1241	106.5	3.4	401	2	US-09-248-796A-26759	Sequence 26759, A
1169	108	3.4	705	2	US-09-902-540-11260	Sequence 11260, A	1242	106.5	3.4	420	2	US-09-902-540-13993	Sequence 13993, A
1170	108	3.4	820	2	US-09-252-991A-23346	Sequence 23346, A	1243	106.5	3.4	423	2	US-08-702-665A-5	Sequence 5, Appl
1171	108	3.4	1015	1	US-08-537-210A-1	Sequence 1, Appl	1244	106.5	3.4	464	1	US-08-836-854-19	Sequence 19, Appl
1172	108	3.4	1015	2	US-09-113-825-1	Sequence 1, Appl	1245	106.5	3.4	464	2	US-09-366-009-7	Sequence 7, Appl
1173	108	3.4	1189	2	US-09-287-354-3	Sequence 3, Appl	1246	106.5	3.4	464	2	US-08-809-156B-8	Sequence 8, Appl
1174	108	3.4	1320	2	US-10-164-595-58	Sequence 58, Appl	1247	106.5	3.4	464	2	US-09-775-964-7	Sequence 7, Appl
1175	108	3.4	1404	2	US-10-164-595-78	Sequence 78, Appl	1248	106.5	3.4	489	2	US-09-366-009-8	Sequence 8, Appl
1176	108	3.4	1411	2	US-09-949-016-10827	Sequence 10827, A	1249	106.5	3.4	489	2	US-08-809-156B-8	Sequence 8, Appl
1177	108	3.4	1618	1	US-08-462-467B-4	Sequence 4, Appl	1250	106.5	3.4	489	2	US-09-775-964-8	Sequence 8, Appl
1178	108	3.4	1711	1	US-08-342-930-2	Sequence 2, Appl	1251	106.5	3.4	575	2	US-08-922-865-2	Sequence 2, Appl
1179	108	3.4	2887	2	US-08-462-467B-2	Sequence 2, Appl	1252	106.5	3.4	575	2	US-09-510-949-2	Sequence 2, Appl
1180	108	3.4	4551	2	US-09-320-878-1	Sequence 1, Appl	1253	106.5	3.4	642	2	US-08-872-855-10	Sequence 10, Appl
1181	108	3.4	4551	2	US-09-141-908-2	Sequence 2, Appl	1254	106.5	3.4	974	2	US-10-101-464A-921	Sequence 921, App
1182	108	3.4	4551	2	US-09-657-440-1	Sequence 1, Appl	1255	106.5	3.4	1003	1	US-08-571-758-4	Sequence 4, Appl
1183	108	3.4	4551	2	US-09-793-708-1	Sequence 1, Appl	1256	106.5	3.4	1003	1	US-08-909-984A-4	Sequence 4, Appl
1184	108	3.4	4613	2	US-09-105-537-31	Sequence 31, Appl	1257	106.5	3.4	1075	1	PCT-US94-07297-41	Sequence 41, Appl
1185	107.5	3.4	134	2	US-09-191-647-12	Sequence 12, Appl	1258	106.5	3.4	1185	2	US-09-041-886-23	Sequence 23, Appl
1186	107.5	3.4	134	2	US-09-540-248A-12	Sequence 12, Appl	1259	106.5	3.4	1185	2	US-09-538-092-1209	Sequence 1209, Ap
1187	107.5	3.4	134	2	US-09-540-153-12	Sequence 12, Appl	1260	106.5	3.4	1476	2	US-09-252-991A-29427	Sequence 29427, A
1188	107.5	3.4	134	2	US-10-289-776-12	Sequence 12, Appl	1261	106.5	3.4	1507	2	US-09-914-259-37	Sequence 37, Appl
1189	107.5	3.4	260	2	US-09-270-767-46622	Sequence 46622, A	1262	106.5	3.4	2090	2	US-09-538-092-1081	Sequence 1081, Ap
1190	107.5	3.4	305	2	US-09-252-991A-22096	Sequence 22096, A	1263	106.5	3.4	2120	2	US-09-949-016-9768	Sequence 9768, Ap
1191	107.5	3.4	328	2	US-09-252-991A-21969	Sequence 21969, A	1264	106.5	3.4	2453	2	US-09-632-033B-4	Sequence 4, Appl
1192	107.5	3.4	374	2	US-09-252-991A-28527	Sequence 28527, A	1265	106.5	3.4	2940	2	US-10-226-629A-13	Sequence 13, Appl
1193	107.5	3.4	419	2	US-09-630-155-2	Sequence 2, Appl	1266	106.5	3.4	3594	2	US-09-911-842A-4	Sequence 4, Appl
1194	107.5	3.4	459	2	US-08-470-335-239	Sequence 239, App	1267	106.5	3.4	115	2	US-09-621-976-4566	Sequence 4266, Ap
1195	107.5	3.4	459	2	US-08-467-602-299	Sequence 299, App	1268	106	3.4				

1269	106	3.4	173	2	US-10-101-464A-741	Sequence 741, App	1342	106	3.4	1244	2	US-08-480-474-46	Sequence 46, Appl
1270	106	3.4	254	2	US-09-252-991A-21433	Sequence 21433, A	1343	106	3.4	1244	2	US-08-940-086A-46	Sequence 46, Appl
1271	106	3.4	259	2	US-10-104-047-3858	Sequence 3858, Ap	1344	106	3.4	1244	2	US-08-940-035A-46	Sequence 46, Appl
1272	106	3.4	370	2	US-09-252-991A-18438	Sequence 18438, A	1345	106	3.4	1244	2	US-08-935-105A-46	Sequence 46, Appl
1273	106	3.4	421	2	US-09-902-540-14807	Sequence 14807, A	1346	106	3.4	1244	2	US-09-648-797-46	Sequence 46, Appl
1274	106	3.4	448	2	US-09-949-016-10130	Sequence 10130, A	1347	106	3.4	1244	2	US-09-386-123-46	Sequence 46, Appl
1275	106	3.4	503	2	US-09-248-796A-18992	Sequence 18992, A	1348	106	3.4	1244	2	US-10-038-937-46	Sequence 46, Appl
1276	106	3.4	531	2	US-10-104-047-2775	Sequence 2775, Ap	1349	106	3.4	1244	2	US-10-007-747-46	Sequence 46, Appl
1277	106	3.4	666	2	US-09-050-739-70	Sequence 70, Appl	1350	106	3.4	1244	2	US-09-945-901-46	Sequence 46, Appl
1278	106	3.4	732	2	US-09-134-000C-6359	Sequence 6359, Ap	1351	106	3.4	1958	1	US-07-945-283-2	Sequence 2, Appl
1279	106	3.4	762	1	US-08-642-255-120	Sequence 120, App	1352	106	3.4	2185	2	US-09-854-856-36	Sequence 36, Appl
1280	106	3.4	763	1	US-08-397-633A-31	Sequence 31, Appl	1353	106	3.4	2185	2	US-10-010-720-36	Sequence 36, Appl
1281	106	3.4	762	3	US-09-949-016-10382	Sequence 10382, A	1354	106	3.4	2245	2	US-09-854-856-4	Sequence 4, Appl
1282	106	3.4	830	2	US-08-872-855-11	Sequence 11, Appl	1355	106	3.4	2245	2	US-10-010-720-4	Sequence 4, Appl
1283	106	3.4	1209	2	US-09-949-002-493	Sequence 493, App	1356	106	3.4	2322	2	US-09-854-856-34	Sequence 34, Appl
1284	106	3.4	1209	2	US-09-949-002-494	Sequence 494, App	1357	106	3.4	2322	2	US-10-010-720-34	Sequence 34, Appl
1285	106	3.4	1214	1	US-08-231-193A-54	Sequence 54, Appl	1358	106	3.4	2382	2	US-09-854-856-2	Sequence 2, Appl
1286	106	3.4	1214	1	US-08-486-273A-54	Sequence 54, Appl	1359	106	3.4	2382	2	US-10-010-720-2	Sequence 2, Appl
1287	106	3.4	1214	2	US-08-480-474-54	Sequence 54, Appl	1360	106	3.4	2743	2	US-10-037-182-36	Sequence 36, Appl
1288	106	3.4	1214	2	US-08-940-086A-54	Sequence 54, Appl	1361	106	3.4	2647	2	US-09-949-016-10932	Sequence 10932, A
1289	106	3.4	1214	2	US-08-940-035A-54	Sequence 54, Appl	1362	106	3.4	3695	2	US-10-037-182-2	Sequence 2, Appl
1290	106	3.4	1214	2	US-08-935-105A-54	Sequence 54, Appl	1363	105.5	3.4	175	2	US-09-325-932A-186	Sequence 186, App
1291	106	3.4	1214	2	US-09-648-797-54	Sequence 54, Appl	1364	105.5	3.4	301	2	US-09-252-991A-17405	Sequence 17405, A
1292	106	3.4	1214	2	US-09-386-123-54	Sequence 54, Appl	1365	105.5	3.4	457	2	US-09-774-639-108	Sequence 108, App
1293	106	3.4	1214	2	US-10-038-937-54	Sequence 54, Appl	1366	105.5	3.4	486	2	US-09-538-092-1269	Sequence 1269, Ap
1294	106	3.4	1214	2	US-10-007-747-54	Sequence 54, Appl	1367	105.5	3.4	486	2	US-09-949-016-6151	Sequence 6151, Ap
1295	106	3.4	1214	2	US-09-945-901-54	Sequence 54, Appl	1368	105.5	3.4	510	2	US-08-246-489-2	Sequence 2, Appl
1296	106	3.4	1219	1	US-08-231-193A-50	Sequence 50, Appl	1369	105.5	3.4	559	2	US-10-116-370-2	Sequence 2, Appl
1297	106	3.4	1219	1	US-08-486-273A-50	Sequence 50, Appl	1370	105.5	3.4	567	2	US-09-949-016-10952	Sequence 2, A
1298	106	3.4	1219	2	US-08-480-474-50	Sequence 50, Appl	1371	105.5	3.4	574	2	US-09-062-440-2	Sequence 2, Appl
1299	106	3.4	1219	2	US-08-940-086A-50	Sequence 50, Appl	1372	105.5	3.4	574	2	US-09-712-495-2	Sequence 2, Appl
1300	106	3.4	1219	2	US-08-940-035A-50	Sequence 50, Appl	1373	105.5	3.4	695	2	US-09-538-092-1152	Sequence 1152, Ap
1301	106	3.4	1219	2	US-08-935-105A-50	Sequence 50, Appl	1374	105.5	3.4	695	2	US-09-949-016-6102	Sequence 6102, Ap
1302	106	3.4	1219	2	US-09-648-797-50	Sequence 50, Appl	1375	105.5	3.4	713	2	US-09-949-016-11425	Sequence 11425, A
1303	106	3.4	1219	2	US-09-386-123-50	Sequence 50, Appl	1376	105.5	3.4	749	2	US-09-949-016-8645	Sequence 8645, Ap
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1309	106	3.4	1231	2	US-08-480-474-48	Sequence 48, Appl	1382	105.5	3.4	766	2	US-09-949-016-11357	Sequence 11358, A
1310	106	3.4	1231	2	US-08-940-086A-48	Sequence 48, Appl	1383	105.5	3.4	766	2	US-09-949-016-11358	Sequence 11359, A
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1316	106	3.4	1231	2	US-10-007-747-48	Sequence 48, Appl	1389	105.5	3.4	2410	2	US-09-270-767-44775	Sequence 44775, A
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1321	106	3.4	1236	2	US-08-940-086A-6	Sequence 6, Appl	1394	105	3.3	422	2	US-09-151-102-2	Sequence 2, Appl
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1327	106	3.4	1236	2	US-10-007-747-6	Sequence 6, Appl	1400	105	3.3	476	2	US-09-252-991A-21580	Sequence 21580, A
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1330	106	3.4	1239	1	US-08-486-273A-52	Sequence 52, Appl	1403	105	3.3	511	2	US-08-473-446-17	Sequence 17, Appl
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1332	106	3.4	1239	2	US-08-940-086A-52	Sequence 52, Appl	1405	105	3.3	631	2	US-09-252-991A-20063	Sequence 20063, A
1333	106	3.4	1239	2	US-08-940-035A-52	Sequence 52, Appl	1406	105	3.3	645	2	US-10-104-047-3418	Sequence 3418, Ap
1334	106	3.4	1239	2	US-08-935-105A-52	Sequence 52, Appl	1407	105	3.3	726	2	US-09-252-991A-20675	Sequence 20675, A
1335	106	3.4	1239	2	US-09-648-797-52	Sequence 52, Appl	1408	105	3.3	811	2	US-09-252-991A-28570	Sequence 28570, A
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1338	106	3.4	1239	2	US-10-007-747-52	Sequence 52, Appl	1411	105	3.3	885	1	US-09-949-016-7789	Sequence 7789, Ap
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QY 541 GFCAGPLELEGVKVPLEPGPKATEGGGEALPGSGSCEVPLMGFPGLQSPHAKPYI 598  
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RESULT 2

US-09-944-457-69  
; Sequence 69, Application US/099444457  
; Patent No. 6734288  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,457  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
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; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-944-457-69

Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 6.6e-217;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 3

US-09-945-584-69  
; Sequence 69, Application US/09945584  
; Patent No. 6908993  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,584  
; PRIOR FILING DATE: 2001-09-26  
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; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
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; PRIOR FILING DATE: No. 6908993ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6908993ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
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; PRIOR APPLICATION NUMBER: PCT/US00/05841  
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; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-945-584-69

Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 6.6e-217;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 LTYRNLSGDKRLVTLRLPASLAETVTLQRLRNATYSVCVMPGLGPRVPEGEACGEAHT 480  
Db 421 LTYRNLSGDKRLVTLRLPASLAETVTLQRLRNATYSVCVMPGLGPRVPEGEACGEAHT 480  
QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRRGRAMAAAAQDKGV 540  
Db 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRRGRAMAAAAQDKGV 540  
QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPGSSECEVPLMGFPGQLQSPHLHAKPYI 598  
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPGSSECEVPLMGFPGQLQSPHLHAKPYI 598

RESULT 4  
US-09-944-944-69  
; Sequence 69, Application US/09944944  
; Patent No. 6929947  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tuma, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,944  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/216,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6929947ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6929947ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT

1

ORGANISM: Homo Sapien  
US-09-944-944-69

Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 6.6e-217;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLALGPGVQCPCGCGCQSQQTVCCTARQQTTPRDPVPPDTGLYVP 60  
DB 1 MCSRVPLLLPLLLLALGPGVQCPCGCGCQSQQTVCCTARQQTTPRDPVPPDTGLYVP 60

QY 61 ENGITWLDASSFAGLGLQQLDLSQNIASLRPLRLLLDLSHNSLLEPEGLDTPANVE 120  
DB 61 ENGITWLDASSFAGLGLQQLDLSQNIASLRPLRLLLDLSHNSLLEPEGLDTPANVE 120

QY 121 ALRLAGLGLQQLDEGLFSLRLNHLDDVSDNQLRVPVIRGLRGLRTRLRAGNTRIAQL 180  
DB 121 ALRLAGLGLQQLDEGLFSLRLNHLDDVSDNQLRVPVIRGLRGLRTRLRAGNTRIAQL 180

QY 181 RPEDLAGLAALQBLDVSNLSQALPGDLGSLFPRLRLAAARNPFCVPLSMFGPWVRE 240  
DB 181 RPEDLAGLAALQBLDVSNLSQALPGDLGSLFPRLRLAAARNPFCVPLSMFGPWVRE 240

QY 241 SHVTLASPETRCHFPFKNAGRLILLEDYADFQCPATTTATVPTTRPVVREPTALSSSL 300  
DB 241 SHVTLASPETRCHFPFKNAGRLILLEDYADFQCPATTTATVPTTRPVVREPTALSSSL 300

QY 301 APTWLSPTAPATEAPSPPTAPPTVGPVPODCCPSTCLNGTCHLGRHHLACI-CPEG 360  
DB 301 APTWLSPTAPATEAPSPPTAPPTVGPVPODCCPSTCLNGTCHLGRHHLACI-CPEG 360

QY 361 FTGLYCESQMGQTRSPPTVTPRPRSLTLGIEPVSPSTSLRVGLQRYLQSSSVQLRSUR 420  
DB 361 FTGLYCESQMGQTRSPPTVTPRPRSLTLGIEPVSPSTSLRVGLQRYLQSSSVQLRSUR 420

QY 421 LTYRNLGSDPKRLVTLRLPASLAETVTOIRPNATYSVCVMPILGCRVPEGEACGEANT 480  
DB 421 LTYRNLGSDPKRLVTLRLPASLAETVTOIRPNATYSVCVMPILGCRVPEGEACGEANT 480

QY 481 PPAVSHNAPVTQAREGNPLIAPALAAVLAALAAVCAACVRRGRAMAAAOQKGV 540  
DB 481 PPAVSHNAPVTQAREGNPLIAPALAAVLAALAAVCAACVRRGRAMAAAOQKGV 540

QY 541 GFGAGPLEGKVKVPLEPGPKATEGGGEALPSSGECEVLMGFGPGGLQSPHAKPYI 598  
DB 541 GFGAGPLEGKVKVPLEPGPKATEGGGEALPSSGECEVLMGFGPGGLQSPHAKPYI 598

RESULT 5  
US-09-945-587-69  
Sequence 69, Application US/09945587  
Patent No. 6936254  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Botstein, David  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Kljavin, Ivar  
APPLICANT: Napier, Mary  
APPLICANT: Roy, Margaret  
APPLICANT: Tumas, Daniel  
APPLICANT: Wood, William  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P2548PIC1  
CURRENT APPLICATION NUMBER: US/09/945,587

1

CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 09/866,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/067,411  
PRIOR FILING DATE: December 3, 1997  
PRIOR APPLICATION NUMBER: 60/069,334  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,335  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,278  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,425  
PRIOR FILING DATE: December 12, 1997  
PRIOR APPLICATION NUMBER: 60/069,696  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,694  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,702  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,870  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/069,873  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/068,017  
PRIOR FILING DATE: December 18, 1997  
PRIOR APPLICATION NUMBER: 60/070,440  
PRIOR FILING DATE: January 5, 1998  
PRIOR APPLICATION NUMBER: 60/074,086  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/074,092  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/075,945  
PRIOR FILING DATE: February 25, 1998  
PRIOR APPLICATION NUMBER: 60/112,850  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 60/113,296  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 60/146,222  
PRIOR FILING DATE: July 28, 1999  
PRIOR APPLICATION NUMBER: PCT/US98/19330  
PRIOR FILING DATE: September 16, 1998  
PRIOR APPLICATION NUMBER: PCT/US98/25108  
PRIOR FILING DATE: December 1, 1998  
PRIOR APPLICATION NUMBER: 09/216,021  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 09/218,517  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 09/254,311  
PRIOR FILING DATE: March 3, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: June 22, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: September 15, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28409  
PRIOR FILING DATE: No. 6936254ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: No. 6936254ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28301  
PRIOR FILING DATE: December 1, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: December 16, 1999  
PRIOR APPLICATION NUMBER: PCT/US00/03565  
PRIOR FILING DATE: February 11, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: February 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: March 2, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/08439  
PRIOR FILING DATE: March 30, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: May 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: July 28, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6 6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLALGPGVQCGSPGCGSQPQTVCFTARQGTTPRDPVPTVGLYVF 60
Db 1 MCSRVPLLLPLLLLALGPGVQCGSPGCGSQPQTVCFTARQGTTPRDPVPTVGLYVF 60
QY 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNSLLALEPGILDANVE 120
Db 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNSLLALEPGILDANVE 120
QY 121 ALRLAGLGLQDDEGLFSLRLNLDLVDSDNQLERVPVIRGLGLTRLRLAGNTRIAQL 180
Db 121 ALRLAGLGLQDDEGLFSLRLNLDLVDSDNQLERVPVIRGLGLTRLRLAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPNCVPLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPNCVPLSWFGPWVRE 240
QY 241 SHVTLASPETRCHFPKPKNAGRLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPETRCHFPKPKNAGRLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGTCHLGRHHLACLCPBG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGTCHLGRHHLACLCPBG 360
QY 361 FTGLYCESQMGQGTSPSTPTTPRPRSLTLGIEPVSPSTSLRVGLQRYLQGSVVQLRSLR 420
Db 361 FTGLYCESQMGQGTSPSTPTTPRPRSLTLGIEPVSPSTSLRVGLQRYLQGSVVQLRSLR 420
QY 421 LTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGRVPEGEACGEAHT 480
Db 421 LTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGRVPEGEACGEAHT 480
QY 481 PPAVHSHNAPVTOAREGNPLLIAPALAAVLLAAAGAAVCVRRGRAMAAAOQKGV 540
Db 481 PPAVHSHNAPVTOAREGNPLLIAPALAAVLLAAAGAAVCVRRGRAMAAAOQKGV 540
QY 541 GPGAGPLEGKVKVPLEPGPKATGEGEALPSGSECEVPLMGFPGLQSPHLHAKPYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATGEGEALPSGSECEVPLMGFPGLQSPHLHAKPYI 598

RESULT 6
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-063-950-2
Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;
QY 1 MCSRVPLLLPLLLLALGPGVQCGSPGCGSQPQTVCFTARQGTTPRDPVPTVGLYVF 60
Db 1 MCSRVPLLLPLLLLALGPGVQCGSPGCGSQPQTVCFTARQGTTPRDPVPTVGLYVF 60
QY 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNSLLALEPGILDANVE 120
Db 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNSLLALEPGILDANVE 120
QY 91 -----LRJPRLLLDLSHNS 105
Db 121 RGLRLRLRYLGKNRIRHIQPCAFDTLDRLLLELKLQDNELRALPPRLRLPRLLLLDLSHNS 180
QY 106 LLALPEGLDITANVEALRLAGLGLQDDEGLFSLRLNLDLVDSDNQLERVPVIRGLRG 165
Db 181 LLALPEGLDITANVEALRLAGLGLQDDEGLFSLRLNLDLVDSDNQLERVPVIRGLRG 240
QY 166 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPF 225
Db 241 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPF 300
QY 226 NCVCLSWFGPWVRESHVTLASPETRCHFPKPKNAGRLLELDYADFGCPATTTATVPT 285
Db 301 NCVCLSWFGPWVRESHVTLASPETRCHFPKPKNAGRLLELDYADFGCPATTTATVPT 360
QY 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGTGC 345
Db 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGTGC 420
QY 346 HLGRHHLACLCPBGFTGLYCESQMGQGTSPSTPTTPRPRSLTLGIEPVSPSTSLRVGL 405
Db 421 HLGRHHLACLCPBGFTGLYCESQMGQGTSPSTPTTPRPRSLTLGIEPVSPSTSLRVGL 480
QY 406 QRYLQGSVVQLRSLRLLTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGP 465
Db 481 QRYLQGSVVQLRSLRLLTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGP 540
QY 466 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNPLLIAPALAAVLLAAAGAAVCV 525
Db 541 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNPLLIAPALAAVLLAAAGAAVCV 600
QY 526 RGRAMAAAOQKGVQPGAGPLEGKVKVPLEPGPKATGEGEALPSGSECEVPLMGFP 585
Db 601 RGRAMAAAOQKGVQPGAGPLEGKVKVPLEPGPKATGEGEALPSGSECEVPLMGFP 660
QY 586 PGLQSPHLHAKPYI 598
Db 661 PGLQSPHLHAKPYI 673

RESULT 7
US-09-991-181-52
; Sequence 52, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C53  
CURRENT APPLICATION NUMBER: US/09/991,181  
CURRENT FILING DATE: 2001-11-16  
PRIORITY APPLICATION NUMBER: 60/049787  
PRIORITY FILING DATE: 1997-06-16  
PRIORITY APPLICATION NUMBER: 60/062250  
PRIORITY FILING DATE: 1997-10-17  
PRIORITY APPLICATION NUMBER: 60/065186  
PRIORITY FILING DATE: 1997-11-12  
PRIORITY APPLICATION NUMBER: 60/065311  
PRIORITY FILING DATE: 1997-11-13  
PRIORITY APPLICATION NUMBER: 60/066770  
PRIORITY FILING DATE: 1997-11-24  
PRIORITY APPLICATION NUMBER: 60/075945  
PRIORITY FILING DATE: 1998-02-25  
PRIORITY APPLICATION NUMBER: 60/078910  
PRIORITY FILING DATE: 1998-03-20  
PRIORITY APPLICATION NUMBER: 60/083322  
PRIORITY FILING DATE: 1998-04-28  
PRIORITY APPLICATION NUMBER: 60/084600  
PRIORITY FILING DATE: 1998-05-07  
PRIORITY APPLICATION NUMBER: 60/087106  
PRIORITY FILING DATE: 1998-05-28  
PRIORITY APPLICATION NUMBER: 60/087607  
PRIORITY FILING DATE: 1998-06-02  
PRIORITY APPLICATION NUMBER: 60/087609  
PRIORITY FILING DATE: 1998-06-02  
PRIORITY APPLICATION NUMBER: 60/087759  
PRIORITY FILING DATE: 1998-06-02  
PRIORITY APPLICATION NUMBER: 60/087827  
PRIORITY FILING DATE: 1998-06-03  
PRIORITY APPLICATION NUMBER: 60/088021  
PRIORITY FILING DATE: 1998-06-04  
PRIORITY APPLICATION NUMBER: 60/088025  
PRIORITY FILING DATE: 1998-06-04  
PRIORITY APPLICATION NUMBER: 60/088026  
PRIORITY FILING DATE: 1998-06-04  
PRIORITY APPLICATION NUMBER: 60/088028  
PRIORITY FILING DATE: 1998-06-04  
PRIORITY APPLICATION NUMBER: 60/088029  
PRIORITY FILING DATE: 1998-06-04  
PRIORITY APPLICATION NUMBER: 60/088030  
PRIORITY FILING DATE: 1998-06-04  
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PRIORITY FILING DATE: 1998-06-04  
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PRIORITY FILING DATE: 1998-06-04  
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PRIORITY FILING DATE: 1998-06-05  
PRIORITY APPLICATION NUMBER: 60/088202  
PRIORITY FILING DATE: 1998-06-05  
PRIORITY APPLICATION NUMBER: 60/088212  
PRIORITY FILING DATE: 1998-06-05  
PRIORITY APPLICATION NUMBER: 60/088217  
PRIORITY FILING DATE: 1998-06-05  
PRIORITY APPLICATION NUMBER: 60/088655  
PRIORITY FILING DATE: 1998-06-09  
PRIORITY APPLICATION NUMBER: 60/088734  
PRIORITY FILING DATE: 1998-06-10  
PRIORITY APPLICATION NUMBER: 60/088738  
PRIORITY FILING DATE: 1998-06-10  
PRIORITY APPLICATION NUMBER: 60/088742  
PRIORITY FILING DATE: 1998-06-10  
PRIORITY APPLICATION NUMBER: 60/088810  
PRIORITY FILING DATE: 1998-06-10  
PRIORITY APPLICATION NUMBER: 60/088824  
PRIORITY FILING DATE: 1998-06-10  
PRIORITY APPLICATION NUMBER: 60/088826  
PRIORITY FILING DATE: 1998-06-10  
PRIORITY APPLICATION NUMBER: 60/088858  
PRIORITY FILING DATE: 1998-06-11  
PRIORITY APPLICATION NUMBER: 60/088861  
PRIORITY FILING DATE: 1998-06-11  
PRIORITY APPLICATION NUMBER: 60/088876  
PRIORITY FILING DATE: 1998-06-11  
PRIORITY APPLICATION NUMBER: 60/089105  
PRIORITY FILING DATE: 1998-06-12  
PRIORITY APPLICATION NUMBER: 60/089440  
PRIORITY FILING DATE: 1998-06-16  
PRIORITY APPLICATION NUMBER: 60/089512  
PRIORITY FILING DATE: 1998-06-16  
PRIORITY APPLICATION NUMBER: 60/089514  
PRIORITY FILING DATE: 1998-06-16  
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PRIORITY FILING DATE: 1998-06-17  
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PRIORITY FILING DATE: 1998-06-17  
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PRIORITY FILING DATE: 1998-06-17  
PRIORITY APPLICATION NUMBER: 60/089599  
PRIORITY FILING DATE: 1998-06-17  
PRIORITY APPLICATION NUMBER: 60/089600  
PRIORITY FILING DATE: 1998-06-17  
PRIORITY APPLICATION NUMBER: 60/089653  
PRIORITY FILING DATE: 1998-06-17  
PRIORITY APPLICATION NUMBER: 60/089801  
PRIORITY FILING DATE: 1998-06-18  
PRIORITY APPLICATION NUMBER: 60/089907  
PRIORITY FILING DATE: 1998-06-18  
PRIORITY APPLICATION NUMBER: 60/089908  
PRIORITY FILING DATE: 1998-06-18  
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PRIORITY FILING DATE: 1998-06-19  
PRIORITY APPLICATION NUMBER: 60/089948  
PRIORITY FILING DATE: 1998-06-19  
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PRIORITY FILING DATE: 1998-06-19  
PRIORITY APPLICATION NUMBER: 60/090246  
PRIORITY FILING DATE: 1998-06-22  
PRIORITY APPLICATION NUMBER: 60/090252  
PRIORITY FILING DATE: 1998-06-22  
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PRIORITY FILING DATE: 1998-06-22  
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QY	466	GRV	P	E	G	E	E	A	C	G	E	A	525
Db	541	GRV	P	E	G	E	E	A	C	G	E	A	600
QY	526	RGR	A	M	A	A	A	A	A	A	A	A	585
Db	601	RGR	A	M	A	A	A	A	A	A	A	A	660
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Db	661	PGL	Q	S	P	L	H	A	K	P	Y	I	673

RESULT 8

US-09-990-444-52

Sequence 52, Application US/09990444

Patent No. 6930170

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730PIC19

CURRENT APPLICATION NUMBER: US/09/990,444

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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72	PRIOR APPLICATION NUMBER: 60/091982	
73	PRIOR FILING DATE: 1998-07-07	

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; PRIOR FILING DATE: 1998-07-09

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Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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Db 1 MCSRVPLLLPALLLALGFGVCGCGSCQCSQOTVCTARQGTTPRDRVPPDTVGLYVF 60
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QY 61 ENGITWLDASSFAGLPGQLLLDSQNOJAS----- 90
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Db 61 ENGITWLDAGSFAGLPGQLLLDSQNOJASLPSGVQFPLANSJLDTANRLRHEITNETF 120
   |||||
QY 91 -----LRLPRLLLLLSHNS 105
   |||||
Db 121 RGLRRLRLYLGNRIHQPCAFDTDLRLLEKLQDNELRALPRLRLPRLLLLLSHNS 180
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QY 106 LLALRPGILDTANVLRALRAGLQLOLDGLSRRLNHLHDVSDNQLERVPPVIRGLRG 165
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Db 181 LLALRPGILDTANVLRALRAGLQLOLDGLSRRLNHLHDVSDNQLERVPPVIRGLRG 240
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QY 166 LTRRLAGNTRIAQLRPEDLAGLALQELDVSNLSIQALPGDLGSLFPRRLRLAAARNPF 225
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RESULT 9

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US-09-997-333-52
; Sequence 52, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC27
; CURRENT APPLICATION NUMBER: US/09/997.333
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-07-09

Query Match          98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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Db 61 ENGITMLDAGSFAGLPGQLLDLSQNIAS----- 90
Qy 91 ----- 105
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; Sequence 52, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; CURRENT APPLICATION NUMBER: US/09/992,598
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; Patent No. 6689866  
; GENERAL INFORMATION:  
; APPLICANT: Shimketa, Richard A.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY  
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides  
; CURRENT APPLICATION NUMBER: US/09520,781  
; CURRENT FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: USSN 60/123,667  
; PRIOR FILING DATE: 1999-03-09  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.0  
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-10

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Db 506 -----VPATD-----TTDKMOTSLDEVKTK-----II 529
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; Patent No. 6942992
; GENERAL INFORMATION:
; APPLICANT: Shimketa, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-10

Query Match      10.7%; Score 337; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

QY 7 LLLPLLLL-----LALGPGVQCPSGCCS-QPOTVCTARQGTTPRDVDPD 53
Db 17 ILLPFVYLTAQWILCAIAAASAGPQNCSCNQFSKVCTRRGLSEVPQIPSN 76
QY 54 TVGLYVFENGITMLDASSFAGLPGQLLDLSQNOIASLR-----LPRLLLLDLSHNSIL 107
Db 77 TRYLMNMENNIQMIQADTFRHLHLEVLQLGKNSIRQIEVGAENGLASLSTLELFDNMLT 136
QY 108 ALEPGILDAN-----VEALRLAGLG-----LQQLDEGLFSRLR 141
Db 137 VIPSGAFEYLSKRLRLNPNPIESIPYAFNRVPSLMRLDLGELKLEYISEGAFEGLF 196
QY 142 N-----LHLDVSDNQLERV-PPVIRGLRGLTRLRAGNTRIA 178
Db 197 NLKYLNLGMCNIKOMPNTPLVGLBELEMSGNHPEIRPGSFHGLSSLKLVWM-NSQVS 255
QY 179 QLRPEDLAGLAALQELDVNSLSQALPGDLGSLFPLRLALAA---RNPFCVCPLSWFG 235
Db 256 LIERNAPDGLASLVELNLAHNLSLPHD---LFTPLRYLVLELHLPNPNWNCDDILMLA 312
QY 236 PWRRESHVTLASPEETRCHFPKNAAGRLLELDYADFCGPATTTTATVTPTRPVVREPTA 295
Db 313 WMLRE-YIPTNSTCCGRCHAPMHRGRYLVVDQASFOCSA-----PFIMDAPRDLNI 364
QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTVGPVPQP-----QDCPPSTC 339
Db 365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHARHPRISVLNDGTLNFHSHVLLSDTGVTY 424
QY 340 -----LNGGTCHLGRHHLACLCPGFTGLYCESOMGQGRPSPTVTP-- 383
Db 425 MGTNVAGNSNASAYLNGSTAEINTSNY-----SFFTGTGETTEISPEDTTRY 473
QY 384 RPPRSLTGLIEPVSTSLRVGLQRYLOGSSVQLRSLRLYRNLSGPDKRLVTLRLPASLA 443
Db 474 KPVPSTTSGYQPAYTTSTTVLIQ-----TTRVPKQVA 505
QY 444 EYTVTLRPNATYSVCMPLGPRVPEGEAEACGEAHTPPAVHSNHPVTOAREGNLPLLI 503
Db 506 -----VPATD-----TTDKMOTSLDEVKTK-----II 529
QY 504 APALAAVLLAALAAVGAAYCYVRR---GRAMAAAAQDKGVGPGAGPLEGKVPLEPGP 560
Db 530 IGCFAVVTLLAAAMLIVFYKLRKHQQRSTVTAAR-----TVEIIQVD-EDIP 576
QY 561 KATEGGGEALPSG 573
Db 577 AATSAATAAPSG 589

RESULT 12
US-09-957-187-10
; Sequence 10, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimketa, Richard A.
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
```

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; TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
;
; FILE REFERENCE: 15966-540 CON S-10
;
; CURRENT APPLICATION NUMBER: US/09/991,053
;
; CURRENT FILING DATE: 2001-11-21
;
; PRIOR APPLICATION NUMBER: USSN 60/123,667
;
; PRIOR FILING DATE: 1993-03-09
;
; PRIOR APPLICATION NUMBER: 09/520,781
;
; PRIOR FILING DATE: 2000-03-08
;
; NUMBER OF SEQ ID NOS: 81
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 10
;
; LENGTH: 653
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; US-09-991-053-10

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Query Match	10.7%	Score 337	DB 2	Length 653
Best Local Similarity	23.6%	Pred. No. 5.1e-16		
Matches	159	Conservative 77	Mismatches 231	Indels 206
Gaps	25			
Qy	7	LLPLLL	-----LALPGVGQCPSCGQCS-QPQTVECTARQCTTVPRDVPD	53
Db	17	ILFPVYLTQWILCAAIAAASAGPQNCPSVCSCNQFSKVYCTRGJSEVPQGPSPN	76	
Qy	54	TUGLYVPENGITMLDASSFAGLQGLQLLDLSQNOIASLR-----LPRLLLDLSHNSLL	107	
Db	77	TRYLNLMENNIQMIQADTFRHLHLEVLQLGKNSIRQIEVCAFNGLASLSTLELFDNWL	136	
Qy	108	ALSPGILDYAN-----VEALRLAGL-----LQQLDEGLFSLRL	141	
Db	137	VIPSGAFEYLSKLRELMLRNPIESIPSYAFNRVPFLMRDLGLKLELVISEGAFGLF	196	
Qy	142	N-----LHLDLDVSDNQLERV-PPVIRGLGLTRLRAGNTRIA	178	
Db	197	NLKYLNLMGNCIIMKMPNLTPLVGLEELMSGNHPEIRPGSFHGLSLKKLWLM-NQSVS	255	
Qy	179	QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLPFRLRLAAA---RNPFCVCPLSWFG	235	
Db	256	LIERNAPDGLASLVELNLAHNNLSLPHD--LFTPLRYLVELHLHNPWNCDDILWLA	312	
Qy	236	PWVRESHVTLASPEETRCHPPKNAGHLLLELDYADFGCPATTTATVPTTRPVVRBP	295	
Db	313	WWLRE-YIPTNSTCCGRCHAPMHRMGRYLVEVDQASFCSA-----PFIMDAPRLNI	364	
Qy	296	LSSSLAP-----TWLSAPTA-TEAPSPSTAPTPTGVPQP-----QDCPSTC	339	
Db	365	SEGRMAELKCRTPPMSSVKVLLPNGTVLSHASRHPRI-SVINDGTLPFSHLLSTGYVTC	424	
Qy	340	-----LNGGTCHLGTRHHLALCLCPGFTGLYCESQMGCTRSPPTVPTP--	383	
Db	425	MGTNVAGNSNASAYLNGSTAEINTSY-----SFFTGTGETTEISPEDTRKY	473	
Qy	384	RPPRSITLGHIEPVSPTSRLRVGLQRYLOGSSVQLRSLSLTVRNLSGPKRLVTLRLPASLA	443	
Db	474	KPVPTTSTGYQPAYTSTTVLIQ-----TTVRPKQVA	505	
Qy	444	EYTVTQLRPNATYSVCVMPILGPGVPSGEACGEAHTPPAVHSNHAPVYQAREGNPLLI	503	
Db	506	-----VPAID-----TTDKQMTSLDEVMKTK-----II	529	
Qy	504	APALAAVLLAALAAGAAAYCVR-----GRAMAAAAQDKGVGPGAGPLEGKVPPLBPGP	560	
Db	530	IGCFVAVTLAAMLIYFYKLKREHQORSTVTAAR-----TWELIQVD-EDIP	576	
Qy	561	KATEGGGEALPSG	573	
Db	577	AATSAATAAPSG	589	

RESULT 14  
US-09-520-781-12  
; Sequence 12, Application US/09520781  
; Patent No. 6689866

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; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-12

Query Match      10.6%; Score 333, DB 2; Length 590;
Best Local Similarity 25.8%; Pred. No. 8,7e-16;
Matches 130; Conservative 60; Mismatches 187; Indels 126; Gaps 18;

Qy   7 LILPLLLLL-----LALPGVGQCPCSCQS-QPQTVCFTARQTTTVPRDVPPD 53
    :|::|:
Db   17 ILLPFYVLTAAQWILCAATAAASAGPNCPSVCSNSQFVKVCTTRGUSEVPQGIPSN 76
    :|::|:
Qy   54 TVGLXYVFENGITMLDASSFAGLPGQLDLDSQNQIASLR-----LPRLLLDLSHNSLL 107
    :|::|:
Db   77 TRYLNLMENNIQMIOADTFRHLHHLEVLQGRNSIRQIEVGAFNGLASLTLEFDNWLT 136
    :|::|:
Qy   108 ALDPGLIDTAN-----VEAIRLAGLG----LQOLDDEGLFSRLR 141
    :|::|:
Db   137 VIPSGAFEYLKRELWLRRNPPIESIPSYAFNRVPISMRDLDELKKLEYISEGAPEGLF 196
    :|::|:
Qy   142 N-----LHDVDSDNQLERV-PPVIRGLRGLTRLRLAGNTRIA 178
    :|::|:
Db   197 NLKYNLGMCNIKDMFNLTPLVCLSELESNGHFPIRPCSPHGLSSLKXKLWM-NSQVS 255
    :|::|:
Qy   179 QRPEDLAGLAALQEILDVSNLSIQALPDGLSLGFRLRLAAA---RNPNVCVCPLSWFEG 235
    :|::|:
Db   256 LIERNAPDGSLAVELNALHNLSLPHD---LFTPLRYLVELHLHHPNWCDCILWLA 312
    :|::|:
Qy   236 PWVRESHVTLASPEETRCFHFPKNAGRILLLEDYADFGPCATTTTATVTRTPVVREPTA 295
    :|::|:
Db   313 WWLURE-YIPTNSTCCGRCHAPMHMGRGYLVEVDQAQSFQCSA-----PFIMDAERDLNI 364
    :|::|:
Qy   296 LSSSLAP-----TWLSPTAPA-TAEPSPSTAPTTCGPVPQP---QDCPPSTC 339
    :|::|:
Db   365 SEGRMAELKCRTPPMSSVKWWLLPNGVTLSHASHPRIISVLNDGTINFSHVLLSDTGVYTIC 424
    :|::|:
Qy   340 -----LNGGTCHIGLTRHHLACLCEPGFTGLYCSEQMQGGTRPSPTVTP-- 383
    :|::|:
Db   425 MGNTVNAGSNASAYLNGSTAELNTSY-----SFFTGTGETEISPEDITRKY 473
    :|::|:
Qy   384 RPPRSITLGI EVPSPTSRLRVGLQ 406
    :|::|:
Db   474 KPVPETTGTGQPAYTTTSTTVLIQ 496
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RESULT 15
US-09-957-187-12
; Sequence 12, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRocheille, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
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